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(54) Title: GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS			
(57) Abstract			
<p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>			

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Genes involved in tolerance to environmental stress

The present invention relates to molecular biology, in particular plant
5 molecular biology. In particular, the invention relates to improvements of crop
productivity of useful plants. One of the major limitations of crop productivity is the
effect of environmental stress conditions on plant growth and development. An
important goal of molecular biology is the identification and isolation of genes that can
provide resistance or tolerance to such stresses. For agriculture, the creation of
10 transgenic plants containing such genes provides the potential for improving the stress
resistance or tolerance of plants.

Drought, salt loading, and freezing are stresses that cause adverse effects on
the growth of plants and the productivity of crops. The physiological response to these
stresses arises out of changes in cellular gene expression. Expression of a number of
15 genes has been demonstrated to be induced by these stresses (Zhu et al., 1997;
Shinozaki et al., 1996; Thomashow, 1994). The products of these genes can be
classified into two groups: those that directly protect against environmental stresses
and those that regulate gene expression and signal transduction in the stress
response. The first group includes proteins that likely function by protecting cells from
20 dehydration, such as the enzymes required for biosynthesis of various
osmoprotectants, late-embryogenesis-abundant (LEA) proteins, antifreeze proteins,
chaperones, and detoxification enzymes (Shinozaki et al., 1997, Ingram et al., 1996,
Bray et al., 1997). The second group of gene products includes transcription factors,
protein kinases, and enzymes involved in phosphoinositide metabolism (Shinozaki et
25 al., 1997). An overview of the methods known to improve stress tolerance in plants is
also given in Holmberg & Bülow, (1998).

Further studies are definitely needed to give an insight into the mechanisms
involved in the plant response to environmental stress conditions.

The study of plants naturally adapted to extreme desiccation has led to the
30 hypothesis that the genetic information for tolerance to environmental stress conditions
exists in all higher plants. In glycophytes, this information would only be expressed in
seeds and pollen grains which undergo a desiccation process.

The induction of osmotolerance in plants is very important to crop productivity:
30 to 50 % of the land under irrigation is presently affected by salinity. Several lines of
35 evidence also demonstrate that even mild environmental stress conditions throughout
the growth season have a negative impact on plant growth and crop productivity. It is

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for instance known that even minor limitations in water availability cause a reduced photosynthetic rate. Unpredictable rainfall, increase in soil salinity at the beginning and the end of the growing season often result in decreased plant growth and crop productivity. These environmental factors share at least one element of stress and that is water deficit or dehydration. Drought is a significant problem in agriculture today. Over the last 40 years, for example, drought accounted for 74% of the total US crop losses of corn. To sustain productivity under adverse environmental conditions, it is important to provide crops with a genetic basis for coping with water deficit, for example by breeding water retention and tolerance mechanisms into crops so that they can grow and yield under these adverse conditions.

It is an aim of the present invention to provide a new method for screening for plant genes involved in tolerance or resistance to environmental stress.

It is an aim of the present invention to provide new plant genes, more particularly plant genes providing the potential of improving the tolerance to environmental stress conditions in plants.

It is also an aim of the present invention to provide polypeptides encoded by said new plant genes.

It is further an aim of the present invention to provide methods for producing plants with enhanced tolerance or resistance to environmental stress conditions based on said new genes.

It is also an aim of the present invention to provide recombinant polynucleic acids comprising said new genes.

It is further an aim of the present invention to provide plant cells and plants transformed with said new genes.

It is further an aim of the present invention to provide plant cells and plants with enhanced tolerance or resistance to environmental stress conditions.

The present invention relates more particularly to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

It has been found that the transfer of genes from plants which are often difficult to assay for certain characteristics, to lower eukaryotes, such as yeasts and fungi, but

in particular yeast, especially *Saccharomyces*, is relatively-easy to achieve, whereby it has now been shown that the results of testing for tolerance or resistance to environmental conditions in the resulting yeast cells gives a relatively reliable measure of the capability of the inserted coding sequence or gene to induce tolerance or resistance to environmental stress in plants. Thus the expression of polynucleic acid sequences comprising the gene or coding sequence which are responsible for inducing tolerance or resistance to environmental stress conditions can be enhanced in the plant species from which it originates or in any other plant species.

In the present context the term "enhancing" must be understood to mean that the levels of molecules correlated with stress protection in a transformed plant cell, plant tissue or plant part will be "substantially increased" or "elevated" meaning that this level will be greater than the levels in an untransformed plant.

This may be achieved by inducing overexpression of suitable genetic information which is already present, or by any other suitable means of introducing into the plant cell heterologous information resulting in a capability to tolerate or resist environmental stress.

The term "environmental stress" has been defined in different ways in the prior art and largely overlaps with the term "osmotic stress". Holmberg et al., 1998 for instance define different environmental stress factors which result in abiotic stress. Salinity, drought, heat, chilling and freezing are all described as examples of conditions which induce osmotic stress. The term "environmental stress" as used in the present invention refers to any adverse effect on metabolism, growth or viability of the cell, tissue, seed, organ or whole plant which is produced by an non-living or non-biological environmental stressor. More particularly, it also encompasses environmental factors such as water stress (flooding, drought, dehydration), anaerobic (low level of oxygen, CO₂ etc.), aerobic stress, osmotic stress, salt stress, temperature stress (hot/heat, cold, freezing, frost) or nutrients/pollutants stress.

The term "anaerobic stress" means any reduction in oxygen levels sufficient to produce a stress as hereinbefore defined, including hypoxia and anoxia.

The term "flooding stress" refers to any stress which is associated with or induced by prolonged or transient immersion of a plant, plant part, tissue or isolated cell in a liquid medium such as occurs during monsoon, wet season, flash flooding or excessive irrigation of plants, etc.

"Cold stress" and "heat stress" are stresses induced by temperatures which are respectively, below or above, the optimum range of growth temperatures for a

particular plant species. Such optimum growth temperature ranges are readily determined or known to those skilled in the art.

“Dehydration stress” is any stress which is associated with or induced by the loss of water, reduced turgor or reduced water content of a cell, tissue, organ or whole
5 plant.

“Drought stress” refers to any stress which is induced by or associated with the deprivation of water or reduced supply of water to a cell, tissue, organ or organism.

“Oxidative stress” refers to any stress which increases the intracellular level of reactive oxygen species.

10 The terms “salinity-induced stress”, “salt-stress” or similar term refer to any stress which is associated with or induced by elevated concentrations of salt and which result in a perturbation in the osmotic potential of the intracellular or extracellular environment of a cell.

Said salt can be for example, water soluble inorganic salts such as sodium
15 sulfate, magnesium sulfate, calcium sulfate, sodium chloride, magnesium chloride, calcium chloride, potassium chloride etc., salts of agricultural fertilizers and salts associated with alkaline or acid soil conditions.

The transgenic plants obtained in accordance with the method of the present invention, upon the presence of the polynucleic acid and/or regulatory sequence
20 introduced into said plant, attain resistance, tolerance or improved tolerance or resistance against environmental stress which the corresponding wild-type plant was susceptible to.

The terms “tolerance” and “resistance” cover the range of protection from a delay to complete inhibition of alteration in cellular metabolism, reduced cell growth
25 and/or cell death caused by the environmental stress conditions defined herein before. Preferably, the transgenic plant obtained in accordance with the method of the present invention is tolerant or resistant to environmental stress conditions in the sense that said plant is capable of growing substantially normal under environmental conditions where the corresponding wild-type plant shows reduced growth, metabolism, viability,
30 productivity and/or male or female sterility. Methodologies to determine plant growth or response to stress include, but are not limited to height measurements, leaf area, plant water relations, ability to flower, ability to generate progeny and yield or any other methodology known to those skilled in the art.

The terms “tolerance” and “resistance” may be used interchangeably in the
35 present invention.

The methods according to the invention as set out below can be applied to any, higher plant, preferably important crops, preferably to all cells of a plant leading to an enhanced osmotic or any other form of environmental stress tolerance. By means of the embodiments as set out below, it now becomes possible to grow crops with improved yield, growth, development and productivity under environmental stress conditions, it may even become possible for instance to grow crops in areas where they cannot grow without the induced osmotolerance according to the invention.

In order to do a thorough screening for relevant plant genes and/or coding sequences, it is preferred to apply a method according to the invention whereby said cDNA library comprises copies of essentially all mRNA of said plant cell. Probably only coding sequences are sufficient. For the screening of genes involved in environmental stress, it is preferred to use a cDNA library from siliques (fruits, containing the maturing seeds), such as the siliques from *Arabidopsis*, because genes involved in for instance osmotolerance are preferentially expressed in these organs.

Although the genetic information may be introduced into yeast for screening by any suitable method, as long as it is in a functional format long enough for testing of tolerance or resistance to environmental stress conditions, it is preferred for ease of operation to use a well known vector such as a 2 μ plasmid. It is to be preferred to have the coding sequence or the gene under control of a strong constitutive yeast promoter, to enhance good expression of the gene or coding sequence of interest. Strong constitutive yeast promoters are well known in the art and include, but are not limited to the yeast TPI promoter.

The term "gene" as used herein refers to any DNA sequence comprising several operably linked DNA fragments such as a promoter and a 5' untranslated region (the 5'UTR), a coding region (which may or may not code for a protein), and an untranslated 3' region (3'UTR) comprising a polyadenylation site. Typically in plant cells, the 5'UTR, the coding region and the 3'UTR (together referred to as the transcribed DNA region) are transcribed into an RNA which, in the case of a protein encoding gene, is translated into a protein. A gene may include additional DNA fragments such as, for example, introns. As used herein, a genetic locus is the position of a given gene in the genome of a plant.

The present invention more particularly relates to an isolated polynucleic acid obtainable by a method comprising the preparation of a cDNA as set out above comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an

enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.

The term "polynucleic acid" refers to DNA or RNA, or amplified versions thereof, or the complement thereof.

5 The present invention more particularly provides an isolated polynucleic acid obtainable by a method as defined above which encodes a polypeptide as listed in Table 1.

The capacity of an isolated polynucleic acid to confer tolerance or resistance to environmental stress conditions can be tested according to methods well-known in the art, see for example, Grillo et al. (1996), Peassarakli et al. (Editor), Nilsen et al. (1996),
10 Shinozaki et al. (1999), Jones et al. (1989), Fowden et al. (1993) or as described in the appended examples.

The present invention more particularly relates to an isolated polynucleic acid which encodes a homolog of any of the polypeptides as listed in Table 1, which is
15 chosen from:

- (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, or 121, or the complementary strands thereof;
- 20 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- 25 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

30 Said fragment as defined above are preferably unique fragments of said sequences.

The term "hybridizing" refers to hybridization conditions as described in Sambrook (1989), preferably specific or stringent hybridization conditions are aimed at.

Stringent conditions are sequence dependent and will be different in different circumstances. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength and pH) at which
5 50% of the target sequence hybridizes to a perfectly matched probe. Typically, stringent conditions will be those in which the salt concentration is about 0.02 molar at pH 7 and the temperature is at least about 60°C.

In the present invention, genomic DNA or cDNA comprising the polynucleic acids of the invention can be identified in standard Southern blots under stringent
10 conditions using the cDNA sequence shown. The preparation of both genomic and cDNA libraries is within the skill of the art. Examples of hybridization conditions are also given in the Examples section.

The present invention also relates to the isolated polynucleic acids which encode polypeptides which are a homolog of the polypeptides as set out in Table 1
15 useful for the production of plants which are resistant or tolerant to environmental stress conditions.

The present invention also relates to a polynucleic acid comprising at least part of any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or
20 at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121. Preferably, said gene encodes a protein having
25 substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76 or 78. Said part of said gene is preferably a unique part.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25,
30 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%,
35 80% or 85% identical, and most preferably at least 90% or 95% identical to any of

SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121 for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

The present invention particularly relates to an isolated polynucleic acid as defined above, which encodes a plant homolog of yeast DBF2 kinase, more particularly a DBF2 kinase homolog from *Arabidopsis thaliana* termed At-DBF2, which can at least be used to confer enhanced environmental stress tolerance or resistance in plants and yeast.

More preferably, the present invention relates to an isolated polynucleic acid encoding a plant DFB2 kinase, which is chosen from:

- (a) SEQ ID NO 1, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (e) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b), or,
- (c) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

Alternatively, the present invention relates to a polynucleic acid derived from a plant comprising at least part of SEQ ID NO 1, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 1. Preferably said gene encodes a protein

having substantially the same biological activity as the protein having the sequence of SEQ ID NO 2.

The present invention also relates to the use of an isolated polynucleic acid as defined above which encodes a plant HSP 17.6A protein for the production of transgenic plants, more particularly a homolog from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 10 (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 15 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

The present invention also relates to the use of a polynucleic acid comprising at least part of SEQ ID NO 3, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 3. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 4, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

More preferably, the present invention relates to the use of an isolated polynucleic acid as defined above which is chosen from:

- 35 (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;

- 5
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
 - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

10 for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

The present invention preferably relates to the use of a polynucleic acid comprising at least part of any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or at least part of a gene that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more
15 preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, for the production of transgenic plants having enhanced tolerance or resistance to environmental stress conditions.

20 Preferably, said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Said part of said gene is preferably a unique part.

25 According to another preferred embodiment, the present invention relates to an isolated polynucleic acid as defined above, which encodes a protein termed c74, more particularly a plant homolog of c74, even more preferably a c74 from *Arabidopsis thaliana*, which at least can be used to confer enhanced environmental stress tolerance in plants and yeast.

More particularly, the present invention relates to an isolated polynucleic acid as defined above, which is chosen from:

30

- (a) SEQ ID NO 5, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,

5 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

Preferably said sequences according to part (b) hybridize under stringent conditions to the sequences of part (a).

10 The present invention also relates to a polynucleic acid comprising at least part of SEQ ID NO 5, or at least part of a gene having a sequence that is at least 50% identical, preferentially at least 55%, 60%, 65% or 70% identical, more preferably at least 75%, 80% or 85% identical, and most preferably at least 90% or 95% identical to SEQ ID NO 5. Preferably said gene encodes a protein having substantially the same biological activity as the protein having the sequence of SEQ ID NO 6.

15 Two nucleic acid sequences or polypeptides are said to be "identical" according to the present invention if the sequence of nucleotides or amino acid residues, respectively, in the two sequences is the same when aligned for maximum correspondence as described below. The term "complementary to" is used herein to mean that the complementary sequence hybridizes to all or a portion of a given
20 polynucleotide sequence.

Sequence comparisons between two (or more) polynucleic acid or polypeptide sequences are typically performed by comparing sequences of the two sequences over a "comparison window" to identify and compare local regions of sequence similarity. A "comparison window", as used herein, refers to a segment of at least
25 about 20 contiguous positions, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted by the local homology algorithm of Smith and Waterman (1981), by the homology alignment
30 algorithm of Needleman and Wunsch (1970), by the search for similarity method of Pearson and Lipman (1988), by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by visual inspection.

"Percentage of sequence identity" is determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleic acid or polypeptide sequences in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not
5 comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the result by 100 to yield the
10 percentage of sequence identity.

The term "substantial identity" of polynucleic acid or polypeptide sequences means that a polynucleotide sequence comprises a sequence that has at least 60%, 65%, 70% or 75% sequence identity, preferably at least 80% or 85%, more preferably at least 90% and most preferably at least 95 %, compared to a reference sequence
15 using the programs described above (preferably BLAST) using standard parameters. One of skill will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into account codon degeneracy, amino acid similarity, reading frame positioning and the like. Substantial identity of amino acid sequences for these purposes normally means
20 sequence identity of at least 40%, 45%, 50% or 55% preferably at least 60%, 65%, 70%, 75%, 80% or 85% more preferably at least 90%, and most preferably at least 95%. Polypeptides which are "substantially similar" share sequences as noted above except that residue positions which are not identical may differ by conservative amino acid changes. Conservative amino acid substitutions refer to the interchangeability of
25 residues having similar side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and
30 tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. Preferred conservative amino acids substitution groups are: valine-leucine-isoleucine, phenylalanine-tyrosine, lysine-arginine, alanine-valine, and asparagine-glutamine.

Another indication that nucleotide sequences are substantially identical is if two molecules hybridize to each other, or a third nucleic acid, under stringent conditions.

More particularly, the polynucleic acids as used herein will comprise at least part of a DNA sequence which is essentially similar, or, preferentially, essentially identical or identical to one or both of the nucleotide or amino acid sequences corresponding to SEQ ID NO 1 to 121 disclosed herein, more specifically in the nucleotide sequence encoding, or the amino-acid sequence corresponding to the "active domain" of the respective protein or polypeptide.

The polynucleic acid sequences according to the present invention can be produced by means of any nucleic acid amplification technique known in the art such as PCR or conventional chemical synthesis.

For a general overview of PCR see PCR Protocols (Innis et al. (1990)).

Polynucleotides may also be synthesized by well-known techniques as described in the technical literature. See, e.g., Carruthers et al. (1982) and Adams et al. (1983). Double stranded DNA fragments may then be obtained either by synthesizing the complementary strand and annealing the strands together under appropriate conditions, or by adding the complementary strand using DNA polymerase with an appropriate primer sequence.

The present invention more particularly relates to an isolated polypeptide encoded by a polynucleic acid according to any of the polynucleic acids as defined above, or a functional fragment thereof.

The present invention preferably relates to an isolated polypeptide as listed in Table 1 or to an isolated polypeptide encoded by a polynucleic acid isolated as defined above. Preferably, the present invention relates to polypeptides or peptides having at least part of the sequence of any of SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120. Preferably, said part is a unique part and preferably includes the active domain of said polypeptide. Preferably said polypeptide is a recombinant polypeptide.

The term "isolated" distinguishes the protein or polynucleic acid according to the invention from the naturally occurring one.

The present invention also relates to a polypeptide comprising at least part of a polypeptide which is at least 50%, 55%, 60%, 65% identical, preferentially at least 70%, 75% identical, more preferably at least 80% or 85% identical, and most

preferably at least 90% or 95% identical to any of SEQ ID NO NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or 120.

5 The terms "polypeptide" and "protein" are used interchangeably throughout the present description.

Said polypeptide preferably has the ability to confer tolerance or resistance to environmental stress conditions in at least plants, plant parts, plant tissues, plant cells, plant calli or yeast.

10 The term "functional fragment" refers to a fragment having substantially the biological activity of the protein from which it is derived.

The polypeptides of the present invention may be produced by recombinant expression in prokaryotic and eukaryotic engineered cells such as bacteria, yeast or fungi. It is expected that those of skill in the art are knowledgeable in the numerous
15 expression systems available for expression in these systems.

The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell
20 enhances tolerance or resistance to environmental stress of said plant.

The term "plant cell" as defined above also comprises plant tissue or a plant as a whole. The present invention more particularly relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising transiently introducing into a plant cell a recombinant DNA comprising any
25 of the polynucleic acids encoding a protein as listed in Table 1 which when (over)expressed in a plant cell enhances tolerance or resistance to environmental stress in said plant.

The term "(over)expression" refers to the fact that the polypeptides of the invention encoded by said polynucleic acid are preferably expressed in an amount
30 effective to confer tolerance or resistance to the transformed plant, to an amount of salt, heat, cold, (or other stress factors) that inhibits the growth of the corresponding untransformed plant.

Several methods to obtain transient introduction and expression of a recombinant DNA in a plant are known to the art. For example, plant virus vectors can

be used to obtain such purpose. Examples conferring to the use of plant viral vectors are described in Porta and Lomonossoff (1996), WO9320217 and US 5,589,367.

The present invention also relates to a method for producing a plant with enhanced environmental stress resistance or tolerance, said method comprising stably
5 introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids as defined above which when (over)expressed in a plant cell enhances the environmental stress tolerance or resistance of a plant.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method
10 comprising introducing into the genome of a plant cell a recombinant DNA comprising any of the polynucleic acids encoding a protein as listed Table 1 which when (over)expressed in a plant cell enhances the environmental stress resistance of said plant.

According to a preferred embodiment, the present invention relates to a
15 method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a DBF2 kinase, preferably a plant DBF2 kinase, most preferably an Arabidopsis DBF2 kinase.

According to another preferred embodiment, the present invention relates to a
20 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding an HSP 17.6A protein, preferably a plant HSP 17.6A protein, most preferably an Arabidopsis HSP 17.6A.

According to a preferred embodiment, the present invention relates to a
25 method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid as defined above encoding a c74 protein, preferably a plant c74 protein, most preferably a Arabidopsis c74 protein.

Preferably, the present invention relates to a method as defined above,
30 comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid as defined above, and,
- a plant expressible promoter, whereby said
35 polynucleic acid is in the same transcriptional unit

and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein as defined above.

The present invention also relates to a method as defined above, comprising:

(a) introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid or indirectly increases or induces the protein activity of a protein encoded by said polynucleic acid of the present invention, and,
- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter, and,

(b) regenerating said plant from said plant cell.

A "recombinant" DNA molecule will comprise a "heterologous sequence" meaning that said recombinant DNA molecule will comprise a sequence originating from a foreign species, or, if from the same species, may be substantially modified from its original form. For example, a promoter operably linked to a structural gene which is from a species different from which the structural gene was derived, or, if from the same species, may be substantially modified from its original form.

The present invention also relates to a method as defined above for producing a plant with enhanced tolerance or resistance to environmental stress conditions, said method comprising indirectly increasing or inducing the expression of an endogenous gene in said plant comprised within a polynucleic acid as defined above or indirectly increasing or inducing the activity of a protein of the invention as defined above. According to this embodiment, other polynucleic acids modulating the expression or the activity of a protein according to the present invention may be introduced

transiently or stably into the genome of said plants. The term "modulating" means enhancing, inducing, increasing, decreasing or inhibiting.

Increase or induction of expression or induction or increase of protein activity is required when said regulator protein is a positive regulator of the expression or the activity of at least one of the polynucleic acids or protein of the present invention.

Decrease or inhibition of expression or decrease or inhibition of protein activity is required when said regulator protein is a negative regulator of the expression or activity of at least one of the polynucleic acids or proteins of the present invention.

Increase of the activity of said polypeptide according to the present invention is obtained, according to one embodiment of the invention, by influencing endogenous gene expression in the plant. This is preferably achieved by the introduction of one or more polynucleic acid sequences according to the invention into the plant genome, in a suitable conformation for gene expression (e.g. under control of a plant-expressible promoter). This will result in increased or induced expression (overexpression) or increased or induced activity of the protein in the plant cells, and, in the presence of an adequate substrate, in an increase of tolerance or resistance to environmental stress conditions in a transgenic plant or plant cell as compared to a non-transgenic plant or plant cell. This increase in tolerance can be measured by measuring mRNA levels, or where appropriate, the level or activity of the respective protein (e.g. by means of ELISA, activity of the enzyme as measured by any technique known in the art). Endogenous gene expression refers to the expression of a protein which is naturally found in the plant, plant part or plant cell concerned.

Alternatively, said enhanced tolerance or resistance to environmental stress conditions may be achieved by introducing into the genome of the plant, one or more transgenes which interact with the expression of endogenous genes (polynucleic acids) according to the present invention, by anti-sense RNA, co-suppression or ribozyme suppression of genes which normally inhibit the expression of the polynucleic acids of the present invention or by suppression of genes which normally inhibit the activity of the polypeptides of the invention as defined above.

For inhibition of expression, the nucleic acid segment to be introduced generally will be substantially identical to at least a portion of the endogenous gene or genes to be repressed. The sequence, however, need not be perfectly identical to inhibit expression. The vectors of the present invention can be designed such that the inhibitory effect applies to other genes within a family of genes exhibiting homology or substantial homology to the target gene.

For antisense suppression, the introduced sequence also need not be full length relative to either the primary transcription product or fully processed mRNA.

Generally, higher homology can be used to compensate for the use of a shorter sequence.

5 Furthermore, the introduced sequence need not have the same intron or exon pattern, and homology of non-coding segments may be equally effective. Normally, a sequence of between about 30 or 40 nucleotides up to the full length sequence should be used, though a sequence of at least about 100 nucleotides is preferred, a sequence of at least about 200 nucleotides is more preferred, and a sequence of
10 about 500 to about 1700 nucleotides is especially preferred.

Catalytic RNA molecules or ribozymes can also be used to inhibit expression of genes as explained above. It is possible to design ribozymes that specifically pair with virtually any target RNA and cleave the phosphodiester backbone at a specific location, thereby functionally inactivating the target RNA. In carrying out this cleavage,
15 the ribozyme is not itself altered, and is thus capable of recycling and cleaving other molecules, making it a true enzyme. The inclusion of ribozyme sequences within antisense RNAs confers RNA-cleaving activity upon them, thereby increasing the activity of the constructs.

A number of classes of ribozymes have been identified. One class of
20 ribozymes is derived from a number of small circular RNAs which are capable of selfcleavage and replication in plants. The RNAs replicate either alone (viroid RNAs) or with a helper virus (satellite RNAs). Examples include RNAs from avocado sunblotch viroid and the satellite RNAs from tobacco ringspot virus, lucerne transient streak virus, velvet tobacco mottle virus, solanum nodiflorum mottle virus and
25 subterranean clover mottle virus. The design and use of target RNA-specific ribozymes is described in Haseloff et al. (1988).

Another method of suppression of gene expression is sense suppression. Introduction of nucleic acid configured in the sense orientation has been shown to be an effective means by which to block the transcription of target genes. For an example
30 of the use of this method to modulate expression of endogenous genes see, Napoli et al. (1990), and U.S. Patents Nos. 5,034,323, 5,231,020, and 5,283,184.

The suppressive effect may occur where the introduced sequence contains no coding sequence per se, but only intron or untranslated sequences homologous to sequences present in the primary transcript of the endogenous sequence. The
35 introduced sequence generally will be substantially identical to the endogenous

sequence intended to be repressed. This minimal identity will typically be greater than about 65%, but a higher identity might exert a more effective repression of expression of the endogenous sequences. Substantially greater identity of more than about 80% is preferred, though about 95% to absolute identity would be most preferred. As with
5 antisense regulation, the effect should apply to any other proteins within a similar family of genes exhibiting homology or substantial homology.

For sense suppression, the introduced sequence, needing less than absolute identity, also need not be full length, relative to either the primary transcription product or fully processed mRNA. This may be preferred to avoid concurrent production of
10 some plants which are overexpressers. A higher identity in a shorter than full length sequence compensates for a longer, less identical sequence. Furthermore, the introduced sequence need not have the same intron or exon pattern, and identity of non-coding segments will be equally effective. Normally, a sequence of the size ranges noted above for antisense regulation is used.

15 Other methods for altering or replacing genes known in the art can also be used to inhibit expression of a gene. For instance, insertional mutants using T-DNA or transposons can be generated. See, e.g., Haring et al. (1991) and Walbot (1992). Another strategy in genetic engineering of plants and animals is targeted gene replacement. Homologous recombination has typically been used for this purpose
20 (see, Capecchi (1989)).

Alternatively, the present invention also relates to a method as defined above wherein said DNA encodes a sense or antisense RNA or a ribozyme capable of indirectly increasing or inducing the expression of an endogenous polynucleic acid sequence according to the invention as defined above or increasing or inducing the
25 activity of a protein of the invention as defined above. Preferably said endogenous polynucleic acid encodes a protein as listed in Table 1.

The present invention also relates to a recombinant polynucleic acid comprising: a polynucleic acid as defined above, and, a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control
30 of said plant-expressible promoter.

The present invention also relates to a recombinant polynucleic acid comprising:

(a) a DNA encoding a protein which when expressed in said plant at an effective amount indirectly increases or induces the expression of an endogenous

polynucleic acid as defined above or indirectly increases or induces the protein activity of a polypeptide as defined above, and,

(b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.

5 An "endogenous" polynucleic acid refers to a polynucleic acid that is already present in the plant species before transformation.

Said recombinant polynucleic acid as described here above is generally also referred to as a "recombinant vector" or an "expression cassette". An expression cassette of the invention can be cloned into an expression vector by standard
10 methods. The expression vector can then be introduced into host cells by currently available DNA transfer methods.

The present invention also relates to the recombinant polynucleic acid as defined above, comprising a DNA which encodes an anti-sense RNA, a ribozyme or a sense RNA which increases or induces the activity of a protein as defined above in
15 said cell. Preferably said protein is listed in Table 1.

More particularly, the present invention relates to a recombinant polynucleic acid comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99,
20 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121.

Preferably, the present invention relates to a recombinant polynucleic acid comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1. Preferably, said "part" is a unique part of any of said nucleotide sequences. (26-28) As used herein, the term a "plant-expressible promoter" refers to a promoter
25 that is capable of driving transcription in a plant cell. This includes any promoter of plant origin, including the natural promoter of the transcribed DNA sequence, but also any promoter of non-plant origin which is capable of directing transcription in a plant cell. The promoter may also be an artificial or synthetic promoter. The term "plant-expressible promoter" includes, but is not restricted to, constitutive, inducible, organ-,
30 tissue-specific or developmentally regulated promoters.

According to the invention, production and/or activity of a polypeptide according to the present invention in a plant or in plant parts is increased by introducing *one or more* polynucleic acids according to the invention into the genome of the plant. More specifically, the constitutive promoter can be, but is not restricted to, one of the
35 following: a 35S promoter (Odell et al. (1985)), a 35S'3 promoter (Hull and Howell

(1987)), the promoter of the nopaline synthase gene ("PNOS") of the Ti-plasmid (Herrera -Estrella, (1983)) or the promoter of the octopine synthase gene ("POCS", De Greve et al. (1982)). It is clear that other constitutive promoters can be used to obtain similar effects. A list of plant-expressible promoters that can be used according to the present invention is given in Table 2.

For specific embodiments of this invention, the use of inducible promoters can provide certain advantages. Modulation of protein levels or protein activity may be required in certain parts of the plant, making it possible to limit modulation to a certain period of culture or developmental stage of the plant.

For specific embodiments of this invention, the use of organ- or tissue-specific or chemical inducible promoters can provide certain advantages. Thus, in specific embodiments of the invention, the gene(s) or part thereof is (are) placed under the control of a promoter directing expression in specific plant tissues or organs, such as for instance roots, leaves, harvestable parts, etc.

It is also possible to use a promoter that can be induced upon the environmental stress conditions. Such promoters can be taken for example from stress-related genes which are regulated directly by an environmental, i.e. preferable abiotic, stress in a plant cell, including genes for which expression is increased, reduced or otherwise altered. These stress related genes comprise genes the expression of which is either induced or repressed by anaerobic stress, flooding stress, cold stress, dehydration stress, drought stress, heat stress or salinity. An exemplary list of such promoters is given in Table 3.

The recombinant polynucleic acids according to the present invention may include further regulatory or other sequences from other genes, such as leader sequences (e.g. the cab22 leader from Petunia), 3' transcription termination and polyadenylation signals (e.g. from the octopine synthase gene or the nopaline synthase gene), plant translation initiation consensus sequences, introns, transcription enhancers and other regulatory elements such as adh intron 1, etc, which is or are operably linked to the gene or a fragment thereof. Additionally, the recombinant polynucleic acid can be constructed and employed to target the gene product of the polynucleic acid of the invention to a specific intracellular compartment within a plant cell on to direct a protein to the extracellular environment. This can generally be obtained by operably joining a DNA sequence encoding a transit or signal peptide to the recombinant polynucleic acid.

The recombinant DNA comprising one or more polynucleic acids according to the present invention may be accompanied by a chimeric marker gene (Hansen et al., 1999 and references therein). The chimeric marker gene can comprise a marker DNA that is operably linked at its 5' end to a plant-expressible promoter, preferably a constitutive promoter, such as the CaMV 35S promoter, or a light inducible promoter such as the promoter of the gene encoding the small subunit of Rubisco; and operably linked at its 3' end to suitable plant transcription 3' end formation and polyadenylation signals. It is expected that the choice of the marker DNA is not critical, and any suitable marker DNA can be used. For example, a marker DNA can encode a protein that provides a distinguishable color to the transformed plant cell, such as the A1 gene (Meyer et al., (1987)), can provide herbicide resistance to the transformed plant cell, such as the *bar* gene, encoding resistance to phosphinothricin (EP 0 242 246), or can provide antibiotic resistance to the transformed cells, such as the *aac(6')* gene, encoding resistance to gentamycin (WO94/01560).

According to another embodiment, the present invention relates to the use of the polynucleic acids above as selectable marker gene. More preferably, the present invention also relates to the use of the plant DBF2 gene as defined above as selectable marker gene, selection taking place with treatment with a stress condition.

The recombinant DNA vectors according to the present invention comprising the sequences from genes of the invention will typically also comprise a marker gene which confers a selectable phenotype on plant cells. For example, the marker may encode biocide resistance, particularly antibiotic resistance, such as resistance to kanamycin, G418, bleomycin, hygromycin, or herbicide resistance, such as resistance to chlorosulfuron or Basta.

The present invention also relates to a recombinant host cell transformed with an isolated polynucleic acid as defined above. Said host can be any host known in the art. Preferably said recombinant host cell is a plant cell, yeast, fungi, insect cell, etc. In order to be efficiently expressed in said host, said polynucleic acids can be combined with any promoter known to function in said host system. Methods for transforming said host cells are also well known in the art.

The present invention particularly also relates to a plant cell transformed with at least one recombinant polynucleic acid as defined above.

The present invention also relates to a plant consisting essentially of plant cells transformed with at least one recombinant polynucleic acid as defined above.

A "transgenic plant" refers to a plant comprising a transgene in the genome of essentially all of its cells.

DNA constructs of the invention may be introduced into the genome of the desired plant host by a variety of conventional techniques (see for example Hansen et al., 1999 for review and WO 99/05902). For example, DNA constructs of the invention may be introduced into the genome of the desired plant host by using techniques such as protoplast transformation, biolistics or microprojectile bombardment or Agrobacterium mediated transformation.

Microinjection techniques are known in the art and well described in the scientific and patent literature. The introduction of DNA constructs using polyethylene glycol precipitation is described in Paszkowski et al. (1984).

Electroporation techniques are described in Fromm et al. (1985). Biolistic transformation techniques are described in Klein et al. (1987).

Alternatively, the DNA constructs may be combined with suitable T-DNA flanking regions and introduced into a conventional Agrobacterium host vector. The virulence functions of the Agrobacterium host will direct the insertion of the construct and adjacent marker into the plant cell DNA when the cell is infected by the bacteria. Agrobacterium tumefaciens-mediated transformation techniques, including disarming and use of binary vectors, are well described in the scientific literature. See, for example Horsch et al. (1984), and Fraley et al. (1983).

Transformed plant cells which are derived by any of the above transformation techniques can be cultured to regenerate a whole plant which possesses the transformed genotype and thus the desired phenotype. Such regeneration techniques rely on manipulation of certain phytohormones in a tissue culture growth medium. Plant regeneration from cultured protoplasts is described in Evans et al. (1983); and Binding (1985). Regeneration can also be obtained from plant callus, explants, organs, or parts thereof. Such regeneration techniques are described generally in Klee et al. (1987).

The polynucleic acids and polypeptides of the invention can be used to confer desired traits on a broad range of plants, including monocotyledonous or dicotyledonous plants, preferably they belong to a plant species of interest in agriculture, wood culture or horticulture, such as a crop plant, root plant, oil producing plant, wood producing plant, fruit producing plant, fodder or forage legume, companion or ornamental or horticultured plant. The plants can include species from the genera Actinidia, Apium, Allium, Ananas, Arachis, Arisaema, Asparagus, Atropa, Avena, Beta,

Brassica, Carica, Cichorium, Citrus, Citrullus, Capsicum, Cucumis, Cucurbita, Cydonia, Daucus, Diospyros, Fragaria, Glycine, Gossypium, Helianthus, Heterocallis, Hordeum, Hyoscyamus, Ipomoea, Lactuca, Linum, Lolium, Lycopersicon, Malus, Mangifera, Manihot, Majorana, Medicago, Musa, Nicotiana, Oryza, Panicum, 5 Pannesetum, Persea, Petroselinum, Phaseolus, Pisum, Pyrus, Prunus, Raphanus, Rheum, Ribes, Rubus, Saccharum, Secale, Senecio, Sinapis, Solanum, Sorghum, Spinacia, Trigonella, Triticum, Vaccinium, Vitis, Vigna, Zea, and Zingiber. Additional species are not excluded. Crops grown on cultivated lands in arid and semi-arid areas in which irrigation with ground water is needed may advantageously benefit from the 10 invention.

One of skill will recognize that after the recombinant polynucleic acid is stably incorporated in transgenic plants and confirmed to be operable, it can be introduced into other plants by sexual crossing. Any of a number of standard breeding techniques can be used, depending upon the species to be crossed. As described before, the 15 plant cells, plant tissue, in particular, transgenic plants of the invention display a certain higher or enhanced degree of tolerance (or even resistance) to environmental stress conditions compared to the corresponding wild-type plants. For the meaning of "environmental stress", see supra. In a preferred embodiment of the present invention, the transgenic plant displays increased tolerance to osmotic stress, salt stress, cold 20 and/or heat stress. An increase in tolerance to such environmental stress is understood to refer to a tolerance to a level of such stress which inhibits the growth and productivity of the corresponding untransformed plant, as determined by methodologies known to the art. Such increased tolerance in transgenic plants is related to an increased expression level in the transgenic plant or parts thereof of one 25 ore more of the polynucleic acids of the present invention and/or to an increased level of activity of the polypeptide(s) encoded by said polynucleic acid, as determined by methodologies known to the art. In comparison with their untransformed counterparts, and determined according to methodologies known in the art, a transgenic plant according to the present invention shows an increased growth, viability, metabolism, 30 fertility and/or productivity under mild environmental stress conditions. In the alternative, a transgenic plant according to the invention can grow under environmental stress conditions wherein the untransformed counterparts can not grow. An increase in tolerance to salt stress is understood to refer to the capability of the transgenic plant to grow under stress conditions which inhibit the growth of at least 35 95% of the parent, non-stress tolerant plants from which the stress tolerant transgenic

plants are derived. Typically, the growth rate of stress tolerant plants of the invention will be inhibited by less than 50%, preferably less than 30%, and most preferably will have a growth rate which is not significantly inhibited by growth conditions which inhibit the growth of at least 95% of the parental, non-stress tolerant plants. In an alternative
5 example, under mild environmental stress conditions, the growth and/or productivity of the transgenic plants is statistically at least 1 % higher than for their untransformed counterparts, preferably more than 5 % higher and most preferably more than 10 % higher.

Any transformed plant obtained according to the invention can be used in a
10 conventional breeding scheme or in *in vitro* plant propagation to produce more transformed plants with the same characteristics and/or can be used to introduce the same characteristic in other varieties of the same or related species.

Furthermore, the characteristic of the transgenic plants of the present invention to maintain normal/rapid/high growth rates under environmental stress conditions can
15 be combined with various approaches to confer environmental stress tolerance with the use of other stress tolerance genes. Some examples of such stress tolerant genes are provided in Holmberg and Bülow (1998). Most prior art approaches which include the introduction of various stress tolerance genes have the drawback that they result in reduced or abnormal growth (compared to non-transgenic controls) under normal,
20 non-stressed conditions, namely stress tolerance comes at the expense of growth and productivity (Kasuga et al., 1999). This correlation between constitutive expression of stress-responsive genes and reduced growth rates under normal growth conditions indicates the presence of cross talk mechanisms between stress response control and growth control.

Furthermore, the characteristic of the transgenic plants of the present invention to display tolerance to environmental stress conditions can be combined with various
25 approaches to confer to plants other stress tolerance genes, e.g., osmotic protectants such as mannitol, proline; glycine-betaine, water-channeling proteins, etc. Thus, the approach of the present invention to confer tolerance to environmental stress
30 conditions to plants can be combined with prior art approaches which include introduction of various stress tolerance genes. Combination of these approaches may have additive and/or synergistic effects in enhancing tolerance or resistance to environmental stress.

Thus, it is immediately evident to the person skilled in the art that the method of
35 the present invention can be employed to produce transgenic stress tolerant plant with

any further desired trait (see for review TIPTEC Plant Product & Crop Biotechnology 13 (1995), 312-397) comprising:

- (i) herbicide tolerance (DE-A 3701623; Stalker (1988)),
- (ii) insect resistance (Vaek (1987)),
- 5 (iii) virus resistance (Powell (1986), Pappu (1995), Lawson (1996)),
- (iv) ozone resistance (Van Camp (1994)),
- (v) improving the preserving of fruits (Oeller (1991)),
- (vi) improvement of starch composition and/or production (Stark (1992), Visser (1991)),
- 10 (vii) altering lipid composition (Voelker (1992)),
- (viii) production of (bio)polymers (Poirer (1992)),
- (ix) alteration of the flower color, e.g., by manipulating the anthocyanin and flavonoid biosynthetic pathway (Meyer (1987), WO90/12084),
- (x) resistance to bacteria, insects and fungi (Duering (1996), Strittmatter (1995), Estruch (1997)),
- 15 (xi) alteration of alkaloid and/or cardiac glycoside composition,
- (xii) inducing maintaining male and/or female sterility (EP-A1 0 412 006; EP-A1 0 223 399; WO93/25695);
- (xiii) higher longevity of the inflorescences/flowers, and
- 20 (xvi) stress resistance.

Thus, the present invention relates to any plant cell, plant tissue, or plant which due to genetic engineering displays an enhanced tolerance or resistance to environmental stress obtainable in accordance with the method of the present invention and comprising a further nucleic acid molecule conferring a novel phenotype to the plant such as one of those described above.

The present invention also relates to a callus or calli consisting essentially of plant cells as defined here above. Such transgenic calli can be preferably used for the production of secondary metabolites in plant cell suspension cultures.

The present invention also relates to any other harvestable part, organ or tissue or propagation material of the plant as defined here above.

The present invention also relates to the seed of a transgenic plant as defined here above, comprising said recombinant DNA.

The present invention also relates to the use of any isolated polynucleic acid as defined above to produce transgenic plants.

The present invention also relates to the use of a recombinant polynucleic acid as defined above, to produce transgenic plants, preferably transgenic plants having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

5 The present invention also relates to the use of an isolated polynucleic acid as defined above, to produce transgenic callus having an enhanced tolerance or resistance to environmental stress conditions. Preferably said polynucleic acid encodes a polypeptide as listed in Table 1.

10 The present invention also relates to probes and primers derived from the genes of the invention that are useful for instance for the isolation of additional genes having sequences which are similar to but differ from any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, but which encode a protein
15 having substantially the same biological activity as a protein having the amino acids sequence of any of SEQ ID NO 2 to 120 (even numbers) by techniques known in the art, such as PCR. The presence of a homologous gene in another plant species can for instance be verified by means of Northern or Southern blotting experiments.

The present invention also relates to the cloning of the genomic counterpart of
20 any of the cDNA sequences as represented in SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121. These genomic counterparts can be selected from a genomic library using these cDNA sequences as a probe. The present
25 invention also relates to the coding region as well as the promoter region of any of said genomic clones.

The term "probe" according to the present invention refers to a single-stranded oligonucleotide *sequence* which is designed to specifically hybridize to any of the polynucleic acids of the invention.

30 The term "primer" refers to a single stranded oligonucleotide sequence capable of acting as a point of initiation for synthesis of a primer extension product which is complementary to the nucleic acid strand to be copied. Preferably the primer is about 5-50 nucleotides long. The term "target region" of a probe or a primer according to the present invention is a sequence within the polynucleic acid(s) to which the probe or the
35 primer is completely complementary or partially complementary (i.e. with some degree

of mismatch). It is to be understood that the complement of said target sequence is also a suitable target sequence in some cases.

"Specific hybridization" of a probe to a target region of the polynucleic acid(s) means that the probe forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions this probe does substantially not form a duplex with other regions of the polynucleic acids present in the sample to be analysed.

"Specific hybridization" of a primer to a target region of the polynucleic acid(s) means that, during the amplification step, said primer forms a duplex with part of this region or with the entire region under the experimental conditions used, and that under those conditions the primer does not form a duplex with other regions of the polynucleic acids present in the sample to be analysed. It is to be understood that "duplex" as used hereby, means a duplex that will lead to specific amplification.

Preferably, the probes of the invention are about 5 nucleotides to about 1 Kb long, more preferably from about 10 to 25 nucleotides. The nucleotides as used in the present invention may be ribonucleotides, deoxyribonucleotides and modified nucleotides such as inosine or nucleotides containing modified groups which do not essentially alter their hybridization characteristics. The probes according to the present invention preferably include parts of the cDNA sequences of any of the polynucleic acids as defined above.

The present invention also relates to a composition comprising a polynucleic acid sequence as defined above, a polypeptide as defined above, a probe as defined above or a primer as defined above.

The present invention also relates to a pharmaceutical or agrochemical composition comprising said polynucleic acid, a polypeptide of the invention as defined above.

The present invention also relates to antibodies specifically reacting with a protein or polypeptide according to the present invention.

The following Examples describe by way of example the tolerance and/or resistance to several environmental stress conditions observed for transgenic plants and yeast overexpressing some of the polynucleic acids according to the present invention. Unless stated otherwise in the Examples, all recombinant DNA techniques are carried out according to standard protocols as described in Sambrook et al. (1989) and in volumes 1 and 2 of Ausubel et al. (1994). Standard materials and methods for plant molecular work are described in Plant Molecular Biology Labfax (1993) by R.D.D.

Croy, jointly published by BIOS Scientific Publications Ltd. (UK) and Blackwell Scientific Publications, UK.

These examples and figures are not to be construed as limiting to any of the embodiments of the present invention as set out above. All of the references
5 mentioned herein are incorporated by reference.

BRIEF DESCRIPTION OF THE FIGURES AND TABLES

Figure 1. *At-DBF2* encodes a functional homolog of the yeast *Dbf2* (A) Comparison of the deduced amino acid sequence of *At-DBF2* with that of yeast *DBF2*. Gaps were introduced to optimize the alignment. Roman numerals above the *At-DBF2* sequence indicate the protein kinase catalytic subdomains defined by Hanks et al. (1988). (B) Complementation of *dbf2*. The *dbf2* mutant S7-4A [*MATa dbf2Δ::URA3 ura3 leu2 ade5 trp1 his7*] (Toyn and Johnston, 1994) (B1) forms swollen pairs of daughter cells (dumbbells) at restrictive temperature (37°C). The defective morphology of the *dbf2* mutant can be complemented by transformation with the pYX112 centromeric plasmid (Ingenius, R&D system) containing the *At-DBF2* cDNA (B2) or *DBF2* (B3); wild type (CG378 strain, *MATa ade5 leu2 trp1 ura3*) (B4). Log phase cultures were shifted from 28°C to 37°C and photographed after 16 hours. After 16 hours, 98% of the S7-4A cells arrested with a dumbbell morphology (B1) whereas 6,1 and 0% of dumbbells were observed in B1, B3 and B4. Strains were kindly provided by (Dr Lindl, Max Planck Institut für Züchtungsforschung, Köln, Germany).

Figure 2. Overexpression of *DBF2* or *At-DBF2* enhances tolerance to osmotic, salt, heat and cold stress. Yeast cells were grown in YPD and cell density was adjusted to OD600 at 2. (1) DY, (2) DY transformed with pYX212 containing *DBF2*, pYX-YDBF2, (3) DY transformed with vector alone or (4) with vector containing *At-DBF2*, pYX-AtDBF2. Serial dilutions were made in step 1:10. Ten µl of each dilution was spotted on solid YPD medium (control) supplemented with 2M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) or 4µl H₂O₂ (oxidative stress) and incubated at 28°C or at 42°C (heat stress) or at 4°C (cold stress) for 3 days.

Figure 3. *DBF2* and *At-DBF2* are induced by stress. (a) Northern analysis showing the kinetics of *At-DBF2* induction in plants treated with PEG 6000 20 % and the one of *DBF2* in yeast treated with sorbitol 2M for the time indicated. (b) Northern analysis of *At-DBF2* in 10 day-old-plants grown for 5 hours in control conditions (as described in Verbruggen et al. 1993) (1), at 37°C (2), with PEG 6000 20 % (3), NaCl 1% (4), at 4°C (5) or with 0.4 mM H₂O₂ (6); and of *DBF2* in yeast cells grown for 11/2 hour in YPD (1), at 37°C (2), with sorbitol 2M (3), with NaCl 1.2 M (4), at 4°C (5) or with 0.4 mM H₂O₂ (6). Control of loading has been done with EtBr staining and is shown under each Northern analysis.

(c) Western analysis of At-DBF2 in Arabidopsis. Samples are similar to those analysed in (b). Antibodies used were raised against yeast Dbf2 and kindly provided by Dr L. Leindl (Max Planck Institut fur Zuchtungsforschung, Koln, Germany).

5 Figure 4. *DBF2* overexpression can suppress *hog1* osmosensitivity. The *hog1* mutant (4) [W303-1A, *MATa*, *hog1Δ::TRP1*] and wild type (W303) (1) were kindly provided by Dr Thevelein (Katholieke Universiteit Leuven, Belgium). The *hog1* mutant was transformed with pYX-YDBF2 (2) or pYX-AtDBF2 (3). Each of the 4 strains was grown for 16 hours in YPD (rich medium), and cell density was adjusted to
10 OD600 at 2. Serial dilutions, 1:10 were made at five consecutive steps. Ten microliter of each dilution was spotted on solid YPD medium (control) or solid YPD medium supplemented with 0,9 M NaCl and incubated at 28°C for 3 days.

 Figure 5. *T-DBF2* (*Nicotiana tabacum* DBF2) is periodically expressed during
15 plant cell cycle. Tobacco *DBF2* expression has been followed in BY2 cells synchronised with aphidicolin (a & b) or with propyzamide (c & d) with *At-DBF2* as probe. The measure of relative rate of DNA synthesis and of the mitotic index, the use of the cell cycle markers *CYCB1.2* and *H4* markers have been previously described (Reicheld et al., 1995). *T-DBF2* transcript levels were quantified from the blots shown
20 in b and d using a PhosphorImager (Molecular Dynamics).

 Figure 6. shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
25 section) upon applying a salt stress of 200 mM NaCl overnight.

 Figure 7 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left
30 section) upon applying an osmotic stress induced by 20% PEG overnight.

 Figure 8 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left

section) upon applying a cold stress by gradually decreasing the temperature until -7°C .

Figure 9 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section) upon applying a heat stress of 2 hours at 48°C .

Figure 10 shows the results of a comparison of the growth of *A. thaliana* plants transformed with the following constructs: P35S-At-DBF2 (upper left and bottom right section), P35S control (upper right section) and P35S-antisense At-DBF2 (bottom left section). It can be concluded that the P35S-At-DBF2 transformed plants do not show morphological abnormalities compared to the control transgenic plants.

Figure 11 shows the results of a salt stress tolerance test with transgenic *A. thaliana* plants overexpressing HSP 17.6A (A) or c74 (B). The control plants (bottom left in A and B) is a transgenic line transformed with pBIN-35S-CaMVter. The other sections in A are 5 independently obtained transgenic lines overexpressing HSP17.6A. The other sections in B are 5 independently obtained transgenic lines overexpressing c74.

Figure 12 shows the influence of *At-DBF2* expression in sense and antisense orientations on stress tolerance. BY2 cells were transformed by *A. tumefaciens* with recombinant T-DNA vectors containing *At-DBF2* driven by CaMV 35S RNA promoter, pBIN-35S-*At-DBF2* (upper left and right sections in A or diamonds in B), the CaMV 35S promoter and terminator pBIN-35S-CaMVter (bottom left sections in A or triangles in B), or antisense *At-DBF2* under the control of the CaMV 35S promoter pBIN-35S-AS*At-DBF2* (bottom right sections in A or circles in B). (A) Picture of the same amounts of transgenic cells after 3 weeks of growth on solid medium supplemented with 300 mM NaCl, 25% PEG, 2mM H_2O_2 , or at 47°C (heat). (B) Growth of suspension cells in liquid medium. Upon stress, growth was measured as fresh weight and expressed as a percentage of unstressed growth (control) (a). Stresses were applied after subculturing (= day 0) at indicated temperatures (e) and concentrations of NaCl (b) PEG (c), and H_2O_2 (f). For the cold shock (d), cells were maintained at 0°C for 2 days before the 2-week culture at 22°C . For each construction data of three

independent transgenic lines were pooled. To not overload the figure, SDs are not shown (maximum 15% of measured values). (C) Northern analysis of At-DBF2+TDBF2, kin1, and HSP17.6. Total RNAs were extracted from independent lines transformed with pBIN-35S-At-DBF2 (1) and (2), pBIN-35S-CaMter (3), and pBIN-35S-ASAt-DBF2 (4). Osmotic stress was induced with 10% PEG treatment for 5 hr (stressed).

Figure 13 shows the results of the growth of *A. thaliana* plants transformed with p35S-AtHSP17.6A and P35S control (upper right section) upon applying an osmotic stress induced by 20% PEG overnight. The results of two independent experiments are shown, each performed with 3 independently obtained transgenic lines overexpressing At-HSP17.6A (upper left and bottom left and right).

Figure 14 shows the results of the germination of *A. thaliana* plants transformed with p35S-Atc74 and P35S control (bottom section) on mineral medium supplemented with 125 mM NaCl. The results of two independent experiments are shown, each performed with 2 independently obtained transgenic lines overexpressing Atc74 (2 upper sections).

20

Table 1. Classification of the *Arabidopsis thaliana* clones isolated in Example 2. Clones isolated according to the description in example 2 have been analyzed on their potential to confer tolerance. According to the method described in example 2, the tolerance of different yeast transformants expressing an Arabidopsis cDNA to osmotic stress and salt stress was compared with the tolerance of DY wild type cells.

+	:	similar growth to the DY wild type cells;
++	:	growth of the transformant is visible at a 10-fold higher dilution (1:10) than control (1:1);
+++	:	growth of the transformant is visible at a 100-fold higher dilution (1:100) than control (1:1);
++++	:	growth of the transformant is visible at a 1000-fold higher dilution (1:1000) than control (1:1).

Table 2. Exemplary plant-expressible promoters for use in the performance of the present invention.

Table 3. Exemplary stress-inducible promoters for use in the performance of the present invention.

EXAMPLES

Example 1. Construction of the cDNA library.

Total RNA has been isolated from green siliques from *Arabidopsis thaliana* by grinding 1 g of siliques in 4 ml extraction buffer (100 mM tris-HCl, pH 8, 10 mM EDTA, 100 mM LiCl) at 4° C, followed by phenolisation and chloroform: isoamylalcohol (24:1) extraction. To the aqueous phase, LiCl was added up to a final concentration of 2M, and the total RNA was allowed to precipitate overnight at 4°C. After centrifugation, the pellet was redissolved in 400 µl H₂O and reprecipitated with ethanol. Poly(A) messenger RNA was isolated from the total RNA by binding it to an oligo-dT cellulose spun column (Pharmacia), washing the column three times with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA, 0.5 M NaCl and eluting the mRNA with 10 mM Tris-HCl, pH 7.5, 1 mM EDTA at 65° C.

The eluate was precipitated with ethanol, and cDNA was synthesized using MMLV- reverse transcriptase (Pharmacia) and a d(T)₁₄-XhoI primer for the first strand and *E. coli* DNA polymerase I (Pharmacia) for the second strand.

Example 2. Yeast transformation and selection for osmotolerance.

The cDNA was cloned into pYX vectors (Ingenius, R&D systems; 2 µ based pYX 212 for bank 1, ARS/CEN based pYX112 for bank 2) as EcoRI - XhoI fragments, using an Eco RI/Not I adaptor.

In these constructs, the cDNA is under the control of the strong constitutive TPI promoter. The yeast strain DY (MATa, *his3*, *can1-100*, *ade2*, *leu2*, *trp1*, *ura3::3xSV40AP1-lacZ*; kindly provided by N. Jones, Imperial Cancer Research Fund, London, UK) has been transformed with these cDNA libraries, using the Lithium Acetate transformation procedure (Gietz and Schietsl, 1995). After transformation with the Arabidopsis cDNA bank, transformants have been selected for the ability to grow in the presence of 100mM LiCl in a stepwise selection (Lee et al., 1999). LiCl is commonly used for salt tolerance screening in yeast (Haro et al. 1991). Several *A. thaliana* genes, conferring osmotolerance to the yeast, have been isolated (Table 1). To further analyse the potential of the selected Arabidopsis cDNA's to confer tolerance to environmental stress in yeast, each yeast transformant expressing such selected Arabidopsis cDNA's has been exposed to osmotic stress and salt stress. Each of the transformants was therefore grown for 16 hours in YPD (rich medium), and cell density was adjusted to OD₆₀₀ at 2. Serial dilutions, 1:10, were made at three consecutive

steps. Ten microliters of each dilution was spotted on solid YPD medium (control) supplemented with 2 M sorbitol (osmotic stress) or 1.2 M NaCl (salt stress) and incubated at 28°C for 3 days. The results of this drop growth test (see also Lee et al., 1999) are shown in Table 1.

5

Example 3. Characterization of *At-DBF2*.

At-DBF2, a 1.8 kb cDNA (SEQ ID NO 1) has been identified in this screening that encodes a predicted 60.2 kDa protein showing 81 % similarity with the yeast Dbf2 transcriptional regulator. Homology (less than 40% similarity) has also been found with the putative Dbf2 homologues in human, *C. elegans* and *Drosophila* (named Ndr for nuclear Dbf2 related, Millward *et al.* 1995). The *At-DBF2* deduced protein sequence (SEQ ID NO 2) contains the 11 domains of protein kinases (Figure 1A). Amino acids lying between the invariant residues D and N of domain VI do not match the features of serine/threonine specificity (LKPE) defined by Hanks *et al.* (1988) but the GSPDYIALE peptide in domain VIII does well indicate serine/threonine specificity and *At-DBF2* can complement the yeast *dbf2* mutant (Figure 1B).

In mature *Arabidopsis* plants, *At-DBF2* is expressed in all tested organs. The highest abundance of transcripts has been found in siliques. A Southern analysis in *Arabidopsis*, tobacco and tomato has revealed that *DBF2* seems to be conserved in plants (see Example 13 below). As *At-DBF2* has been identified in a screening for LiCl tolerance, its effect in other stress situations has been tested in yeast (Figure 2).

Example 4. Overexpression of *Arabidopsis* and *Saccharomyces cerevisiae* *DBF2* enhances cold, heat, salt and drought tolerance in yeast.

In order to test whether the effect was specific to the plant gene, the yeast *DBF2* gene has been overexpressed in the same vector. Upon a drop growth test (Figure 2 and Lee et al., 1999). A remarkable enhancement of stress tolerance can be seen at 42°C, during osmotic stress (sorbitol), and after salt and cold treatments in yeast. There is no difference between stress tolerance afforded by the plant or the yeast gene. The enhancement of stress tolerance due to the overexpression of *At-DBF2* or *DBF2* reflects a role for these genes in stress situations. Therefore yeast and *Arabidopsis* plants have been exposed to sorbitol- and PEG-induced osmotic stress. *At-DBF2* as well as *DBF2* is induced rapidly (1 to 2 hours) and transiently upon osmotic stress (Figure 3A). The expression of *At-DBF2* and *DBF2* has been analyzed during other environmental stresses in *Arabidopsis* plants or in yeast cells after the

time corresponding to the highest induction seen in Fig. 3A (Figure 3B). In plant as in yeast, there is a clear induction after heat, salt, osmotic and to a lesser extent after cold, which perfectly correlates with stresses to which the overexpression enhances tolerance. However, many genes are induced upon stress without relevant adaptive role, amongst others because post-transcriptional mechanisms inhibit subsequent translation. Here *At-DBF2* protein amount, as detected by anti-Dbf2 antibodies, clearly increased upon stress (Figure 3C).

Example 5. Both *At-DBF2* and *DBF2* can functionally complement the *hog1* mutation.

To investigate a possible interaction between stress signaling pathways and *DBF2*, the salt sensitive *hog1* mutant was transformed with *At-DBF2* and *DBF2*. The *HOG1* MAP kinase pathway regulates osmotic induction of transcription in yeast (Schuller *et al.* 1994). The osmosensitivity of the mutant could be recovered by the overexpression of both *DBF2* and *At-DBF2* (Figure 4).

Example 6. *At-DBF2* is cell cycle regulated.

DBF2 expression is cell cycle regulated where it plays a role in DNA synthesis initiation but also in nuclear division through its association with the CCR4 complex (Komarnitsky *et al.* 1998, Johnston *et al.* 1990). This regulation was investigated in plants. A tobacco BY-2 cell line in which the highest level of culture synchronization, compared with other plant cell lines has been achieved so far (Shaul *et al.* 1996, Reicheld *et al.* 1995) was used. Stationary phase cells were diluted into fresh medium and treated with aphidicolin (blocking cells in the beginning of the S phase) for 24 hours, then washed. The percentage of synchronous mitosis after release from the aphidicolin block was about 65 % (Figure 5A-B). A 1.6-Kb tobacco *DBF2* homologue (*T-DBF2*) could be detected on Northern blot with the *At-DBF2* as a probe. *T-DBF2* steady-state transcript level clearly oscillates during the cell cycle and is mainly present during S, decreases during G2 until late M from where it increases until a peak in S phase. *T-DBF2* expression occurs clearly before *CYCB1.2* (a marker of G2-M phases), but parallels the one of H4 (a S phase marker) except at the S/G2 transition, where *T-DBF2* transcripts decline earlier, and at the M/G1 transition, where *T-DBF2* expression increases earlier. The use of the cell cycle markers *CYCB1.2* and H4 is described in Reicheld *et al.*

To follow unperturbed G1 and S phases, BY2 cell suspension was synchronized using a double blocking procedure (Nagata *et al.*,1992). After the release from the aphidicoline block, cells are treated for 4 hours with propyzamide in the beginning of the preprophase. The percentage of synchronous mitosis after the
5 release from the propyzamide block was higher than 75%. *T-DBF2* was periodically expressed with an undetectable expression until late M, a sharp increase in G1 and a peak in mid S (Figure 5C-D) which confirms results of Figures 5A-B. However a function for the plant *DBF2* in cell cycle can only be assigned with measurement of the kinase activity. In yeast, *DBF2* transcript levels do not correlate with kinase activation
10 which occurs by dephosphorylation (Toyn and Johnson, 1994). The precise function of Dbf2 in regulation of the cell cycle is not known. An essential role has been proposed during anaphase or telophase. No activity has been measured in G1 despite evidence for a role for Dbf2 in initiation of DNA synthesis.

As other proteins recently identified, Dbf2 controls the M/G1 transition
15 which is a major cell cycle transition in yeast (Aerne *et al.* 1998). The existence of a M/G1 control checkpoint has been suggested in plant cells (Hemmerlin and Bach 1998) but its importance compared to G1/S and G2/M has not been investigated.

Overexpression of *DBF2* in yeast results in kinase activity throughout the cell cycle, which may be due to the saturation of a post-translational deactivating
20 mechanism (Toyn and Johnston, 1994). Overexpression of the functionally conserved *At-DBF2* has most probably the same effect. However, the presence of Dbf2 kinase activity at the wrong time in the cell cycle does apparently not affect its progression. In marked contrast constitutive activity has a marked effect on stress tolerance. The role played by *At-DBF2* or *DBF2* in stress is most probably independent from the cell
25 division cycle. *At-DBF2* expression is present in all plant organs (abundant expression is observed in stems where only 1-2 % cells have a mitotic activity) and can be rapidly induced upon stress. However, a link with the cell cycle is not excluded. Higher stress tolerance in yeast overexpressing *DBF2* or *At-DBF2* may be correlated to the overproduction of the kinase in G1 where yeast cells are particularly sensitive to
30 stress. Most plant cells are also thought to be blocked in G1 but the relationship with stress response is poorly known.

Example 7. Tobacco cell transformation and recombinant T-DNA Vector construction

BY2 cells were stably transformed as described (Shaul et al., 1996) by *Agrobacterium tumefaciens* C58C1Rif^R (pGV2260) strain (Deblaere et al., 1985) carrying pBIN-35S-At-DBF2 or pBIN-35S-ASAt-DBF2 recombinant binary vectors. PBIN-35S-At-DBF2 is the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the gfp reporter gene was replaced with a BamHI-SacI fragment containing the At-DBF2 cDNA from pYX-At-DBF2. p-Bin-35S-CaMVter is the plant binary vector pBIN19 in the HindIII-SacI restriction sites of which the hindIII-SacI fragment of pDH51 containing the cauliflower mosaic virus (CaMV) 35S RNA promoter and terminator was cloned. pBIN-35S-ASAt-DBF2 is the pBIN-35S-CaMVter vector in which the At-DBF2 cDNA was cloned in the antisense orientation from pYXAt-DBF2 in the BamHI-SmaI restriction sites, between the CaMV 35S RNA promoter and terminator. More details are described in Lee et al. (1999).

Example 8. Overexpression of At-DBF2 sense and antisense RNA in plant cells

Transgenic plant cells overexpressing *At-DBF2* were generated to test the role of this protein in stress tolerance *in planta*. Tobacco BY2 cells were stably transformed by *A. tumefaciens* carrying the *At-DBF2* cDNA driven by the strong constitutive CaMV 35S RNA promoter. The antisense *At-DBF2* RNA also was overexpressed under the control of the same promoter. Control lines were obtained by transforming tobacco BY2 cells with pBIN-35S-CaMVter. Three independently obtained *At-DBF2*-overexpressing tobacco transgenic cell lines have been selected with a high and similar *At-DBF2* expression and analysed further. Three tobacco transgenic cell lines overexpressing antisense *At-DBF2* were chosen that showed an undetectable tobacco DBF2 transcript level. Both the overexpression of *At-DBF2* and the down-regulation of the endogenous gene by the antisense strategy did not result in significant differences in growth after 2 weeks (Fig. 12A and 12B). On the contrary, marked differences in growth were observed after a 2-week treatment with NaCl, PEG-induced drought, cold, or high temperatures. Transgenic lines that overexpressed *At-DBF2* were clearly more tolerant than control lines. Inhibition of the endogenous DBF2 expression was correlated with a higher sensitivity to those stresses. To understand the basis of stress

tolerance in *At-DBF2*-overexpressing plant cells, expression of stress-induced genes was followed in control and stress conditions (Fig. 12C). Tobacco kin1 and HSP17.6A homologues already were induced in *At-DBF2*-overexpressing tobacco cells in control conditions to a level similar to that observed during stress conditions (PEG-induced drought), suggesting that *At-DBF2* overexpression may mimic a stress signal.

Example 9. Arabidopsis transformation and recombinant T-DNA vector construction with genes conferring tolerance to environmental stress

Arabidopsis were stably transformed as described in Clarke, Wei and Lindsey (1992) by *Agrobacterium tumefaciens* C58C1RifR (pGV2260) strains carrying pBIN-35S-*At-DBF2*, pBIN-35S-*At-HSP17.6A*, pBIN-35S-*At-c74* recombinant binary vectors. pBIN-35S-*At-DBF2* is described in Lee et al. 1999. pBIN-35S-*At-HSP17.6A* recombinant binary vector was constructed as following: the EcoRI-XhoI fragment containing *At-HSP17.6A* cDNA in pYX-HSP17.6A (recombinant pYX212) was first cloned in pYES2 (Invitrogen) resulting in pYES-HSP17.6A. Then the BamHI-SphI fragment of pYES-HSP17.6A containing the *At-HSP17.6A* cDNA was cloned in the plant binary vector pBIN m-gfp4 in which the BamHI-SacI fragment containing the *gfp* receptor gene was deleted and replaced by the *At-HSP17.6A* cDNA. The 3' protruding ends generated by SacI and SphI were blunt ended by T4 DNA polymerase. pBIN-35S-*c74* was constructed with a similar strategy as pBIN-35S-*AtHSP17.6A* with an intermediary pYES-*Atc74* vector. The *At-c74* cDNA was first amplified with PCR using the primers 5' AAA AAA CAC ATA CAG GAA TTC 3' (SEQ ID NO 122) and 5' AGT TAG CTA GCT GAG CTC GAG 3' (SEQ ID NO 123), then cloned "blunt ended" in the vector pYES2 cut with NotI and BstXI and blunt ended with T4 DNA polymerase. Subsequently, the BamHI-SphI fragment of pYES-*c74* was cloned in pBINm-gfp4 as explained supra.

Example 10. Tolerance to environmental stress in plant cells

Transgenic calli were isolated from each of the transgenic Arabidopsis lines transformed with *At-DBF2*, *At-HSP17.6A* and *At-c74*. The growth of these transgenic calli during salt stress was measured and compared with control calli derived from transgenic Arabidopsis lines transformed with pBIN-35S-*CaMVter*. Callus pieces (25 for each transgenic line) of similar fresh weight (50 to 100 mg) were therefor grown on callus inducing medium (Clarke et al., 1992) supplemented with 200mM NaCl. After two weeks, from visual inspection, it was clear that transgenic calli transformed with

At-DBF2 or At-HSP17.6A or At-c74 looked much better than control transgenic calli transformed with pBIN-35S-CaMVter. The latter calli turned yellow and started dying. To confirm the observation, the fresh weight of the calli was measured. In comparison with the control transgenic calli, the fresh weight of the transgenic calli was for each of
5 the three lines at least five times higher than the fresh weight of the control transgenic calli.

Example 11. Tolerance to environmental stress in plants.

Seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2,
10 p-BIN-35S-At-c74, or pBIN-35S-At-HSP17.6A, were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation
15 experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-AS+At-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinstein. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 200 mM NaCl for overnight
20 incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2 or At-HSP17.6A or At-c74 survived very well (Figure 6 and Figure 11).

25 To further evaluate the scope of protection to environmental stress, transgenic plants were exposed to osmotic stress. Therefor seeds from transgenic Arabidopsis plants transformed with pBIN-35S-At-DBF2, pBIN-35S-At-c74 or pBIN-35S-At-HSP17.6A were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For
30 each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance
35 germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark,

70 microeinsteins. After 9 days growth, filters were transferred to liquid K1 medium supplemented with 20 % polyethylene glycol for overnight incubation. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium. Under these conditions, the control transgenic plants turned yellow, their growth was inhibited and eventually they died. On the contrary, the transgenic lines transformed with At-DBF2, At-HSP17.6A or At-c74 survived very well (see Figure 7 and 13). Their growth was comparable to growth on control medium without polyethylene glycol.

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to high and low temperatures. Therefor seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were sown in bulk on nylon filters (as described in Verbruggen et al. 1993) placed on solid K1 medium supplemented with kanamycin (75 micrograms/ml). For each recombinant pBIN binary vector at least five independent transgenic lines were tested for stress tolerance. In each of these lines overexpression of the transgene has been confirmed with Northern hybridisation experiments. Control plants were the ones transformed with pBIN-35S-CaMVter and transgenic plants transformed with pBIN-35S-ASAt-DBF2. After sowing, seeds were kept overnight at 4 degrees (to enhance germination). Growth was at 22 degrees, 60 % humidity, 16 hours light/8 hours dark, 70 microeinsteins. After 9 days growth, for the experiments with high temperature stress, plants were exposed to 48°C for two hours. For the experiments with low temperature stress, plants were exposed to gradually decreasing temperatures, down to -7°C. Plants were allowed to recover for 5 to 6 days by transferring the filters to solid K1 medium.

Under both low temperature and high temperature stress, the growth of control transgenic plants was inhibited and eventually they died. The transgenic lines transformed with At-DBF2 or At-c74 survived very well. Their growth was comparable to growth under control conditions with normal temperature (see Figure 8 and 9).

To further analyse the scope of protection to environmental stress, transgenic plants were exposed to salt stress during germination. Sterilized mature seeds from transgenic plants transformed with pBIN-35S-At-DBF2 or pBIN-35S-At-c74 were placed on top of petri dishes containing MS (Murashige and Skoog) medium with 0,8 % agar and 30 g l⁻¹ sucrose. Control plants were the ones transformed with pBIN-35S-CaMVter. Prior to germination and pH 5.7 adjustment, NaCl was added to a final concentration of 125 mM. Three petri dishes with a mean of 40-50 seeds per dish were used per treatment in every experiment. The complete experiment was repeated

twice. Seed germination at 22°C was followed. Seeds were considered to germinate after radical and green cotyledon emergency occurred.

On control medium (without 125 mM NaCl), germination of all transgenic lines was very similar to each other and to wild type plants. On medium supplemented with 125 mM NaCl, seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate significantly better than control transgenic lines. Less than 10 % of the seeds from transgenic lines transformed with pBIN-35S-CaMVter germinate under these conditions. In contrast, more than 70 % of the seeds from transgenic lines overexpressing At-DBF2 or At-c74 germinate on medium containing 125 mM NaCl (Figure 14).

Example 12. Southern hybridisation of At-DBF2 genes in other plants

To investigate whether *DBF2* homologues exist in other plant species, a Southern hybridisation analysis was performed using the full length *At-DBF2* as a probe. Genomic DNA was extracted from tobacco, tomato and rice according to Dellaporta et al. (1983) and further purified by phenol:chloroform extractions.

DNA (10 µg) was digested with restriction enzymes and separated on 1% (w/v) agarose gels using Lambda DNA digested with Hind III as molecular size standards. The DNA was transferred on to nylon membranes (Hybond N; Amersham, Little Chalfont, UK) in 0.4 N NaOH. Filters were UV-cross-linked for 30 seconds, prehybridized for 3 hours at 56°C in hybridization solution (2x SSPE, 0.1%(w/v) SDS, 5x Denhardt solution) using 200 µg³ denatured salmon sperm DNA, and hybridized overnight with radiolabelled probes. 1X SSPE was 0.15 M NaCl/ 0.01 M sodium dihydrogen phosphate/ 1 mM EDTA

Filters were washed at 56°C in 2x SSPE, 0.1% (w/v) SDS for 20 min, then 1x SSPE, 0.1% (w/v) SDS for 20 min, and finally in 0.1x SSPE, 0.1% (w/v) SDS for 20 min. Filters were exposed to X-ray film (Kodak X-AR; Kodak, NY, USA) in the presence of intensifying screens for 24 hours.

The results of the hybridisation experiments show that tobacco, tomato and rice have at least one homologue to At-DBF2.

Tabel 1

putative function in	Features of encoded protein	SEQ ID NO.	Growth on medium with 1,2 M NaCl	growth on medium with 2,0 M sorbitol
signalling	Similar to a yeast DBF2 cell cycle protein	1	++++	++++
metabolism	HSP17.6A	3	++++	++++
unknown	C74	5	+++	+++
metabolism	Similar to ADH2	7	+	++++
metabolism	Similar to D. melanogaster catalase/catalase 3	9	++++	+
metabolism	Similar to the HSP90 heat shock protein family	11	++++	++++
metabolism	similar to phosphoenolpyruvate carboxylase	13	+	+++
metabolism	pathogen related proteins, class 10	15	+	++++
metabolism	Arabidopsis ascorbate peroxidase	17	++++	++++
metabolism	similar to phosphatase binding protein	19	++++	++++
metabolism	similar to phosphatase binding protein	21	++++	++++
metabolism	similar to retinol dehydrogenase	23	+++	++++
metabolism	similar to retinol dehydrogenase	25	++++	++++
metabolism	ribosomal protein	27	++++	++++
metabolism	ribosomal protein	29	++++	++++
metabolism	similar to a protein transporter (kinase homolog)	31	++++	++++
metabolism	similar to a peptide transporter	33	++++	+
metabolism	similar to a wheat low affinity cation transporter LCT1	35	++++	++++
metabolism	similar to yeast iso-1-cytochrome c (CYC-1)	37	++++	++++
metabolism	similar to yeast OSM1	39	++++	++++
metabolism	similar to yeast copper uptake gene (CUP1)	41	++++	+++
metabolism	similar to yeast UV-induced damage repair protein (RAD7)	43	++++	++++
metabolism	electron transporter, apocytochrome b	45	++++	++++
metabolism	similar to membrane lipoprotein LPPL1	47	++++	++++
metabolism	similar to tobacco auxin binding protein	49	+	++++
metabolism	similar to tobacco cytokinin binding protein CBP 57	51	+++	++++
signalling	similar to calcium binding protein yeast calcineurin B	53	+++	++++

signalling	similar to calcium binding protein glycine max calnexin	55	++++	+++
signalling	similar to calcium binding protein Dictyostelium discoideum calreticulin	57	++++	++++
signalling	similar to calcium binding protein calmodulin 1	59	++++	+
signalling	similar to calcium binding protein calmodulin 2	61	+	++++
signalling	MAP kinase kinase, homologous to Dicytostelium mekA (DdMek1)	63	++++	+++
signalling	similar to human adenosine kinase	65	+	++++
signalling	similar to human tyrosine kinase	67	++++	++++
signalling	similar to common ice plant tyrosine kinase	69	++++	++++
signalling	similar to the yeast protein kinase C receptor	71	++++	++++
signalling	similar to tobacco and Arabidopsis HAT7 homeotic protein	73	++	++++
signalling	similar to E. coli sigma factor regulator (RSEB)	75	+	++++
signalling	similar to human protein phosphatase 2C	77	++++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	79	++	++++
metabolism	late embryogenesis abundant proteins, Arabidopsis LEA protein 10 & 14	81	++	++++
metabolism	pathogen related proteins, class 10	83	++++	++++
metabolism	cell wall peroxidase	85	++++	+++
metabolism	ribosomal protein	87	+++	++++
metabolism	salt stress induced protein, SAS 1	89	++++	++++
metabolism	PR gene (AIG2)	91	++++	++++
metabolism	MT1c	93	++++	++++
metabolism	IPP2 (Isopentenyl diphosphate)	95	+++	++++
metabolism	chlorophyll a/b binding protein	97	+++	+++
metabolism	glutathione transferase	99	++	++++
signalling	cold- and ABA inducible, calcium dependent – kinase, Kin1	101	++++	++++
signalling	MAP kinase, Atmpk1	103	++	++++
signalling	Arabidopsis cell cycle protein histone H2A	105	++++	++++
unknown	chromosome 4 – sequence	107	+++	++++
unknown	chromosome 4 – sequence	109	+	++++
unknown	chromosome 5 – sequence	111	++++	+++
unknown	chromosome 5 – sequence	113	++++	++
unknown	chromosome 5 – sequence	115	++++	++++
unknown	chromosome 5 – sequence	117	+	++++
unknown	chromosome 5 – sequence	119	+	++++

signalling	similar to calcium binding protein centrin (caltractin)	121	++++	++++
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TABLE 2
EXEMPLARY PLANT-EXPRESSIBLE PROMOTERS FOR USE IN THE PERFORMANCE OF
THE PRESENT INVENTION

GENE SOURCE	EXPRESSION PATTERN	REFERENCE
α -amylase (<i>Amy32b</i>)	Aleurone	Lanahan <i>et al</i> (1992); Skriver <i>et al.</i> (1991)
cathepsin β -like gene	Aleurone	Cejudo <i>et al.</i> (1992)
<i>Agrobacterium rhizogenes</i> <i>rolB</i>	Cambium	Nilsson <i>et al.</i> (1997)
PRP genes	cell wall	http://salus.medium.edu/mmg/tierney/html
barley <i>ltr1</i> promoter	Endosperm	
synthetic promoter	Endosperm	Vicente-Carbajosa <i>et al.</i> (1998)
AtPRP4	Flowers	http://salus.medium.edu/mmg/tierney/html
chalcone synthase (<i>chsA</i>)	Flowers	van der Meer <i>et al.</i> (1990)
<i>apetala-3</i>	Flowers	
Chitinase	fruit (berries, grapes, etc)	Thomas <i>et al.</i> CSIRO Plant Industry, Urrbrae, South Australia, Australia; http://winetitles.com.au/qwrdc/csh95-1.html
<i>rbcs-3A</i>	green tissue (eg leaf)	Lam <i>et al.</i> (1990); Tucker <i>et al.</i> (1992)
leaf-specific genes	Leaf	Baszczynski <i>et al.</i> (1988)
AtPRP4	Leaf	http://salus.medium.edu/mmg/tierney/html
<i>Pinus cab-6</i>	Leaf	Yamamoto <i>et al.</i> (1994)
SAM22	Senescent leaf	Crowell <i>et al.</i> (1992)
<i>R. japonicum nif</i> gene	Nodule	United States Patent No. 4, 803, 165
<i>B. japonicum nifH</i> gene	Nodule	United States Patent No. 5, 008, 194

GmENOD40	Nodule	Yang <i>et al.</i> (1993)
PEP carboxylase (PEPC)	Nodule	Pathirana <i>et al.</i> (1992)
Leghaemoglobin (Lb)	Nodule	Gordon <i>et al.</i> (1993)
<i>Tungro bacilliform</i> virus gene	Phloem	Bhattacharyya-Pakrasi <i>et al.</i> (1992)
sucrose-binding protein gene	plasma membrane	Grimes <i>et al.</i> (1992)
pollen-specific genes	pollen; microspore	Albani <i>et al.</i> (1990); Albani <i>et al.</i> (1991)
maize pollen-specific gene	Pollen	Hamilton <i>et al.</i> (1992)
sunflower pollen-expressed gene	Pollen	Baltz <i>et al.</i> (1992)
<i>B. napus</i> pollen-specific gene	pollen; anther; tapetum	Arnoldo <i>et al.</i> (1992)
root-expressible genes	Roots	Tingey <i>et al.</i> (1987); An <i>et al.</i> (1988);
tobacco auxin-inducible gene	root tip	Van der Zaal <i>et al.</i> (1991)
β -tubulin	Root	Oppenheimer <i>et al.</i> (1988)
Tobacco root-specific genes	Root	Conkling <i>et al.</i> (1990)
<i>B. napus</i> G1-3b gene	Root	United States Patent No. 5, 401, 836
SbPRP1	Roots	Suzuki <i>et al.</i> (1993)
AtPRP1; AtPRP3	roots; root hairs	http://salus.mediam.edu/mmg/tierney/html
RD2 gene	root cortex	http://www2.cnsu.edu/ncsu/research
TobRB7 gene	root vasculature	http://www2.cnsu.edu/ncsu/research
AtPRP4	leaves; flowers; lateral root primordia	http://salus.mediam.edu/mmg/tierney/html
Seed-specific genes	Seed	Simon <i>et al.</i> (1985); Scofield <i>et al.</i> (1987); Baszczyński <i>et al.</i> (1990)
Brazil Nut albumin	seed	Pearson <i>et al.</i> (1992)
Legumin	Seed	Ellis <i>et al.</i> (1988)
Glutelin (rice)	Seed	Takaiwa <i>et al.</i> (1986); Takaiwa <i>et al.</i>

		(1987)
Zein	Seed	Matzke <i>et al.</i> (1990)
NapA	Seed	Stalberg <i>et al.</i> (1996)
Sunflower oleosin	seed(embryo and dry seed)	Cummins <i>et al.</i> (1992)
<i>LEAFY</i>	shoot meristem	Weigel <i>et al.</i> (1992)
<i>Arabidopsis thaliana knat1</i>	shoot meristem	Accession number AJ131822
<i>Malus domestica kn1</i>	shoot meristem	Accession number Z71981
<i>CLAVATA1</i>	shoot meristem	Accession number AF049870
Stigma-specific genes	Stigma	Nasrallah <i>et al.</i> (1988); Trick <i>et al.</i> (1990)
Class I patatin gene	Tuber	Liu <i>et al.</i> (1991)
<i>Blz2</i>	Endosperm	EP99106056.7
PCNA rice	Meristem	Kosugi <i>et al.</i> (1991); Kosugi and Ohashi (1997)

Table 3. Stress Inducible promoters

Name	Stress	Reference
P5CS (delta(1)-pyrroline-5-carboxylate syntase)	salt, water	Zhang et al; Plant Science. Oct 28 1997; 129(1): 81-89
cor15a	Cold	Hajela et al., Plant Physiol. 93: 1246-1252 (1990)
cor15b	Cold	Wlihelm et al., Plant Mol Biol. 1993 Dec; 23(5):1073-7
cor15a (-305 to +78 nt)	cold, drought	Baker et al., Plant Mol Biol. 1994 Mar; 24(5): 701-13
rd29	salt, drought, cold	Kasuga et al., Nature Biotechnology, vol 18, 287-291, 1999
heat shock proteins, including artificial promoters containing the heat shock element (HSE)	Heat	Barros et al., Plant Mol Biol, 19(4): 665-75, 1992. Marrs et al., Dev Genet., 14(1): 27-41, 1993. Schoffl et al., Mol Gen Gent, 217(2-3): 246-53, 1989.
smHSP (small heat shock proteins)	heat	Waters et al, J Experimental Botany, vol 47, 296, 325-338, 1996
wcs120	Cold	Ouellet et al., FEBS Lett. 423, 324-328 (1998)
ci7	Cold	Kirch et al., Plant Mol Biol, 33(5): 897-909, 1997 Mar
Adh	cold, drought, hypoxia	Dolferus et al., Plant Physiol, 105(4): 1075-87, 1994 Aug
pws18	water: salt and drought	Joshee et al., Plant Cell Physiol, 39(1): 64-72, 1998, Jan
ci21A	Cold	Schneider et al., Plant Physiol, 113(2): 335-45, 1997
Trg-31	Drought	Chaudhary et al., Plant Mol Biol, 30(6): 1247-57, 1996
Osmotin	Osmotic	Raghothama et al., Plant Mol Biol, 23(6): 1117-28, 1993

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Claims

1. A method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells.
2. An isolated polynucleic acid obtainable by a method according to claim 1.
3. The isolated polynucleic acid of claim 2 which encodes a polypeptide as listed in Table 1.
4. The isolated polynucleic acid of claim 3, which is chosen from:
 - (a) any of SEQ ID NO 1, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77 or 121, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
 - (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
 - (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).
5. The isolated polynucleic acid of any of claim 2 to 4, which encodes a plant homolog of yeast DBF2 kinase.
6. The isolated polynucleic acid of claim 5, which is chosen from:
 - (a) SEQ ID NO 1, or the complementary strands thereof;
 - (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;

- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

5

7. Use of an isolated polynucleic acid of claims 2 to 3 which encodes an HSP 17.6A protein for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

- 10 8. Use of an isolated polynucleic acid of claim 7 for expression of the protein encoded thereby in a plant cell, with said polynucleic acid being chosen from:

- (a) SEQ ID NO 3, or the complementary strand thereof;
- (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- 15 (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
- (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

20

9. Use of an isolated polynucleic acid as defined above which is chosen from:

- (a) any of SEQ ID NO 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, or 119, or the complementary strand thereof;
- 25 (b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
- (c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b) or,
- 30 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c),

- for the production of transgenic plants having an enhanced tolerance or resistance to environmental stress conditions.

35

10. The isolated polynucleic acid of any of claims 2 to 4, which encodes a c74 protein which is chosen from:

- 5 (a) SEQ ID NO 5, or the complementary strand thereof;
(b) polynucleic acid sequences which hybridize to sequences defined in (a) or fragments thereof;
(c) polynucleic acid sequences which are degenerated as a result of the genetic code to the polynucleic acid sequences defined in (a) or (b); or,
10 (d) polynucleic acid sequences encoding a fragment of a protein encoded by a polynucleic acid of any one of (a) to (c).

11. An isolated polypeptide encoded by a polynucleic acid according to or as defined
15 in any of claims 2 to 10, or a functional fragment thereof.

12. The isolated polypeptide of claim 11 having at least part of the sequence of any of
SEQ ID NO 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40,
42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84,
20 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, or
120.

13. A method for producing a plant with enhanced tolerance or resistance to
environmental stress, said method comprising transiently introducing into a plant
25 cell a recombinant DNA comprising a polynucleic acid of or as defined in any of
claims 2 to 10 which is expressed in an amount effective to confer enhanced
tolerance or resistance to environmental stress.

14. A method for producing a plant with enhanced tolerance or resistance to
30 environmental stress, said method comprising stably introducing into a plant cell a
recombinant DNA comprising a polynucleic acid of or as defined in any of claims 2
to 10 which is expressed in an amount effective to confer enhanced tolerance or
resistance to environmental stress.

35

15. The method of claims 13 or 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 5 or 6 encoding a plant DBF2 kinase.

5

16. The method of claim 16 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claims 7 or 8 encoding an HSP 17.6A protein.

10 17. The method of claim 13 to 14 for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into said plant a polynucleic acid of claim 10 encoding a c74 protein.

15 18. The method of any of claims 13 to 17, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a polynucleic acid according to or as defined in any of claims 2 to 10, and,
- a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.

20

19. A method for producing a plant with enhanced tolerance or resistance to environmental stress, comprising introducing into the genome of a plant cell one or more recombinant DNA molecules, said recombinant DNA molecules comprising:

- a DNA encoding a protein which when expressed in said plant cell at an effective amount indirectly increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or indirectly increases or induces the activity of a polypeptide of claims 11 or 12, and,

30

- a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 5 20. A method of claim 19 wherein said DNA encodes a sense or antisense RNA molecule or a ribozyme capable of increasing or inducing the expression of said endogenous polynucleic acid sequence according to or as defined in any of claims 2 to 10.
- 10 21. A recombinant polynucleic acid comprising:
a polynucleic acid according to or as defined in any of claims 2 to 10, and,
a plant expressible promoter, whereby said polynucleic acid is in the same transcriptional unit and under the control of said plant-expressible promoter.
- 15 22. A recombinant polynucleic acid comprising:
(a) a DNA encoding a protein which when expressed in said plant cell at an effective amount increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or increases or induces the activity of a polypeptide of claims 11 or 12, and,
20 (b) a plant expressible promoter, whereby said DNA is in the same transcriptional unit and under the control of said plant-expressible promoter.
23. The recombinant polynucleic acid of claim 22, wherein said DNA encodes an anti-sense RNA, a ribozyme or a sense RNA which when expressed in a cell of a plant
25 increases or induces the expression of an endogenous polynucleic acid according to or as defined in any of claims 2 to 10 or which induces or increases the activity of a protein of claim 11 or 12.
- 30 24. The recombinant polynucleic acid of claim 21 comprising at least part of the nucleotide sequence of any of SEQ ID NO 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 90, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, or 121, or part thereof.

25. The recombinant polynucleic acid of claim 21 to 24 comprising at least part of the coding sequence of a gene encoding a protein as listed in Table 1.
- 5 26. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a constitutive promoter.
27. The recombinant polynucleic acid of any of claims 21 to 25 wherein said plant-expressible promoter is a stress-inducible or organ- or tissue-specific promoter.
- 10 28. The recombinant polynucleic acid of any of claims 21 to 26 wherein said plant-expressible promoter is the 35S promoter of CaMV.
29. A recombinant host cell transformed with at least one isolated polynucleic acid of or as defined in any of claims 2 to 10.
- 15 30. A plant cell transformed with a recombinant polynucleic acid of any one of claims 21 to 28.
31. A plant consisting essentially of plant cells of claim 30.
- 20 32. A callus consisting essentially of plant cells of claim 30.
33. A harvestable part, organ, tissue or propagation material of a plant of claim 31, comprising said recombinant DNA.
- 25 34. The use of a recombinant polynucleic acid of claim 21 to 28 to produce transgenic plants.
- 30 35. A probe which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which hybridizes specifically with said polynucleic acid or the complement thereof.
- 35 36. A primer which is part of the polynucleic acid sequence of or as defined in any of claims 2 to 10 and which specifically amplifies said polynucleic acid or the complement thereof.

37. A composition comprising a polynucleic acid sequence of or as defined in any of claims 2 to 10, a polypeptide of claim 11 or 12, a probe of claim 35 or a primer of claim 36.

At-DBF2MAGNMSCLSTDGHGTPGSGHFPNQNLTKRTRPAGINDSPSPVKCFFFPYEDTSNTSLKEVSQPTKYSSNSPPVSPAIFYERATSWCT	89
DBF2	MLSKSEKNVDLLAGNMSNLSFDGHGTPGGTGLFPNQNTKRTRPAGINDSPSPVKPSFFPYEDTSNMDIDEVSQPDMDVSNPKKLPKPKFYERATSNKT	100
At-DBF2	QRVVSGRAMYFLEYCDMFDYVISRROTKQVLEYLQQQSOLPNSDQIKLNEEUSSYLQREHQVL SKRRLKPKNRD FEMITQVGGGYGHVYLARKKOTK	189
DBF2	QRVVSVCKMYFLEHYCDMFDYVISRROTKQVLEYLQQQSOLPNSDQIKLNEEUSSYLQREHQVL SKRRLKPKNRD FEMITQVGGGYGVVYLARKKOTK	200
At-DBF2	EVCALKILNKKLGLNGTCHVLTERRSLTTTRSETMVKLLSGTTPVGSRGMAIESELGGDFRTESIGRRCLKSGHARFYISEMFCAVNEKHLLSKT...	287
DBF2	EVCALKILNKKLLFKLNETKHVLTERRSLTTTRSEHLVKLLYAFQDLQSLYLAMEFVPGGDFRTLLINTRCLKSGHARFYISEMFCAVNALHDLYGTHRD	300
At-DBF2DSTISNEEDSSINIRLEKFKDLGYPALSEKSIEDRRKLY.....TCPNMSVGSPPDYTALEVLGRKRYEYTVDYHS	356
DBF2	LKPENFLIDAKGHIKLTDFGLAAGTISNERIESMKIRLEKIKOLEFPAFTEKSIEDRRKMYNQLREKEINYANSMVGSPPDYMALEVLGKKYDFTVDYHS	400
At-DBF2	LGCMLFESLVGYTPFGSGSSTNETYATSRWQTLNRARHEDGRAAFYNRTWDLITRHRADLSTRTRSFEHEVKMSYFADILFKALRSIIPPFTPQLDSET	456
DBF2	LGCMLFESLVGYTPFGSGSSTNETYDNLRRWKQTLRRPRQSDGRAAFSDRTWDLITRLIADPINRLRSFEHVKMSYFADINFSTLRSMIPFTPQLDSET	500
At-DBF2	DAGYFDDFWNEADIAKYADVFNQQCRTALVDDSAVSSKLVGFTFRHRNGKGGSSGMLFNGLEHSDPFSTFY	528
DBF2	DAGYFDDFTSEADMAKYADVFKRQDKLTAMVDDSAVSSKLVGFTFRHRNGKGGSSGILFNGLEHSDPFSTFY	572

FIGURE 1 A

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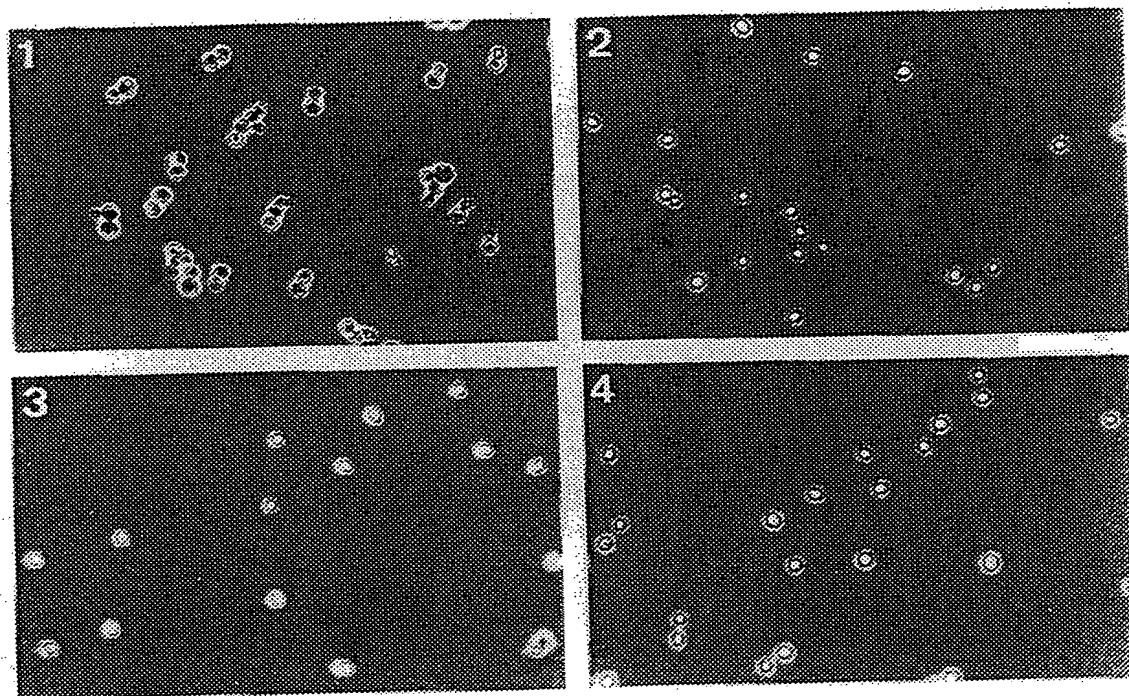


FIGURE 1B

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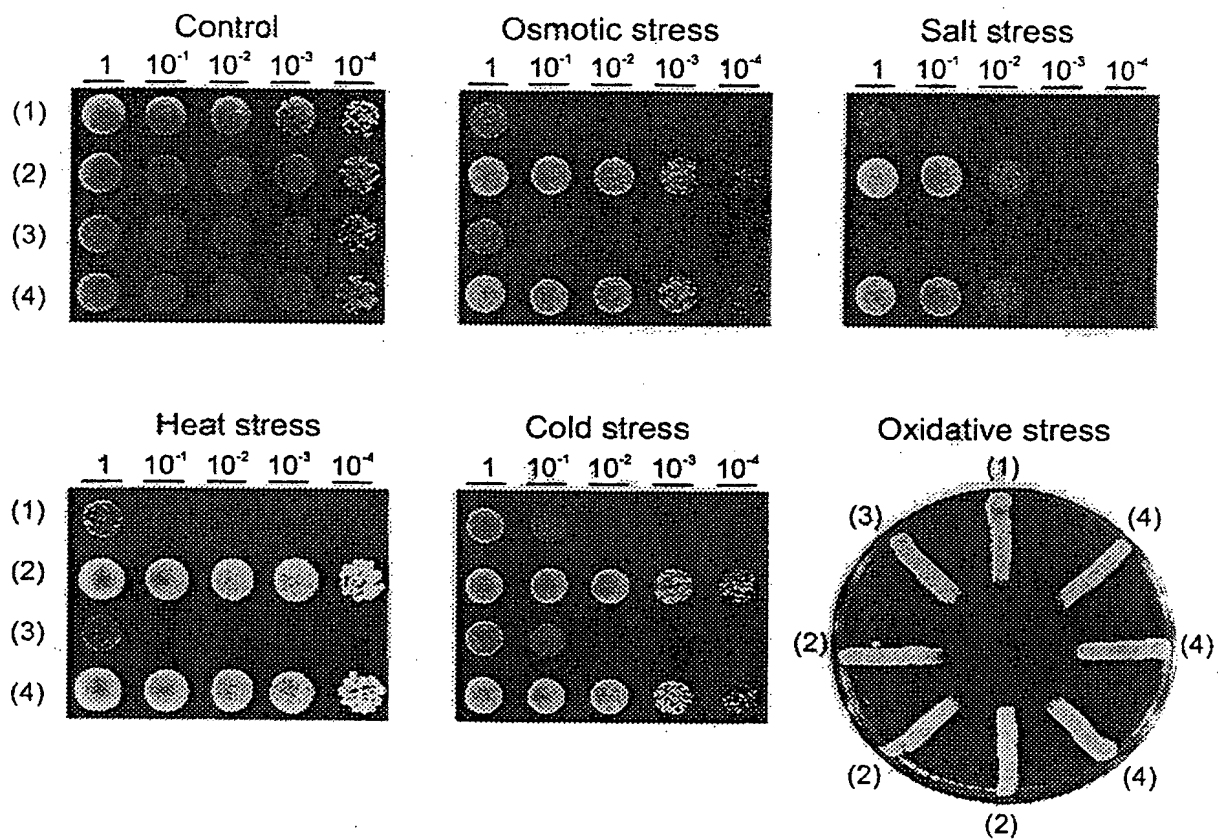


FIGURE 2

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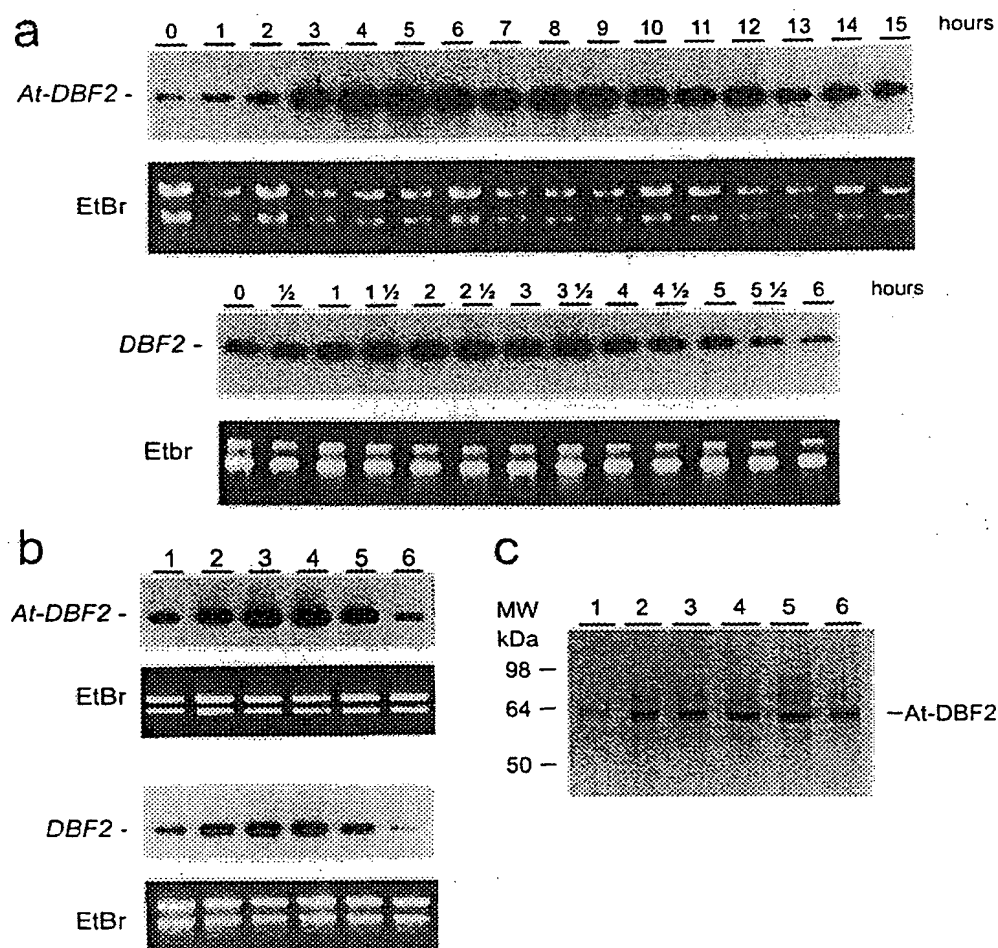


FIGURE 3

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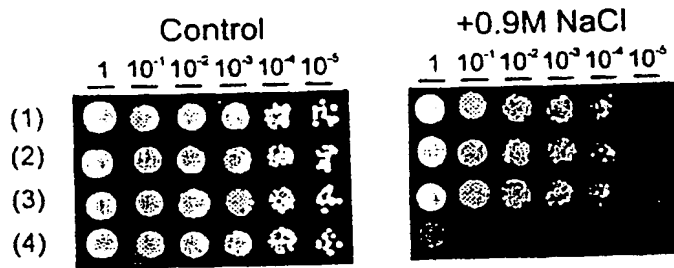


FIGURE 4

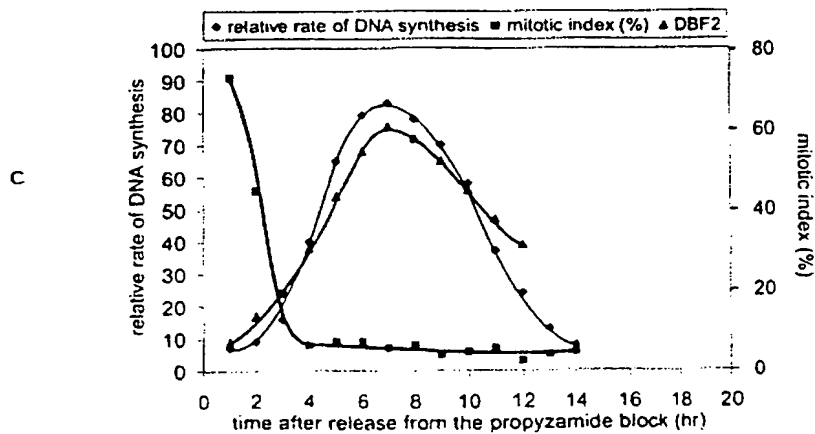
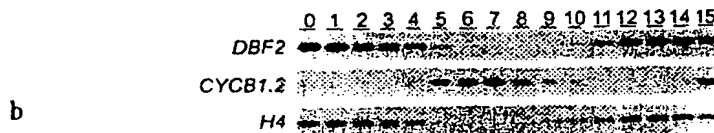
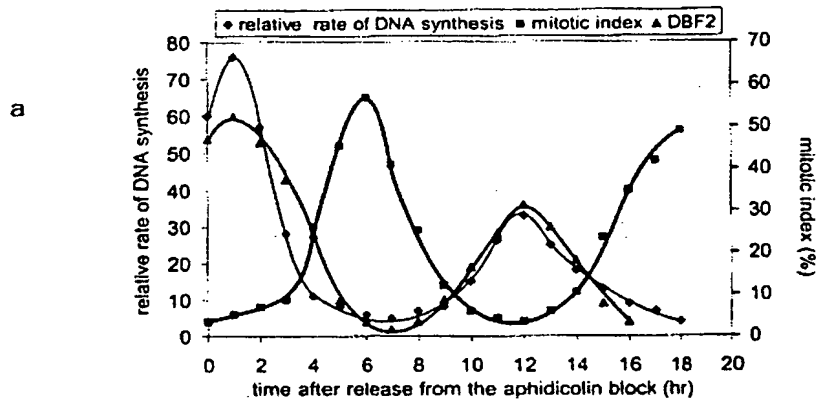


FIGURE 5

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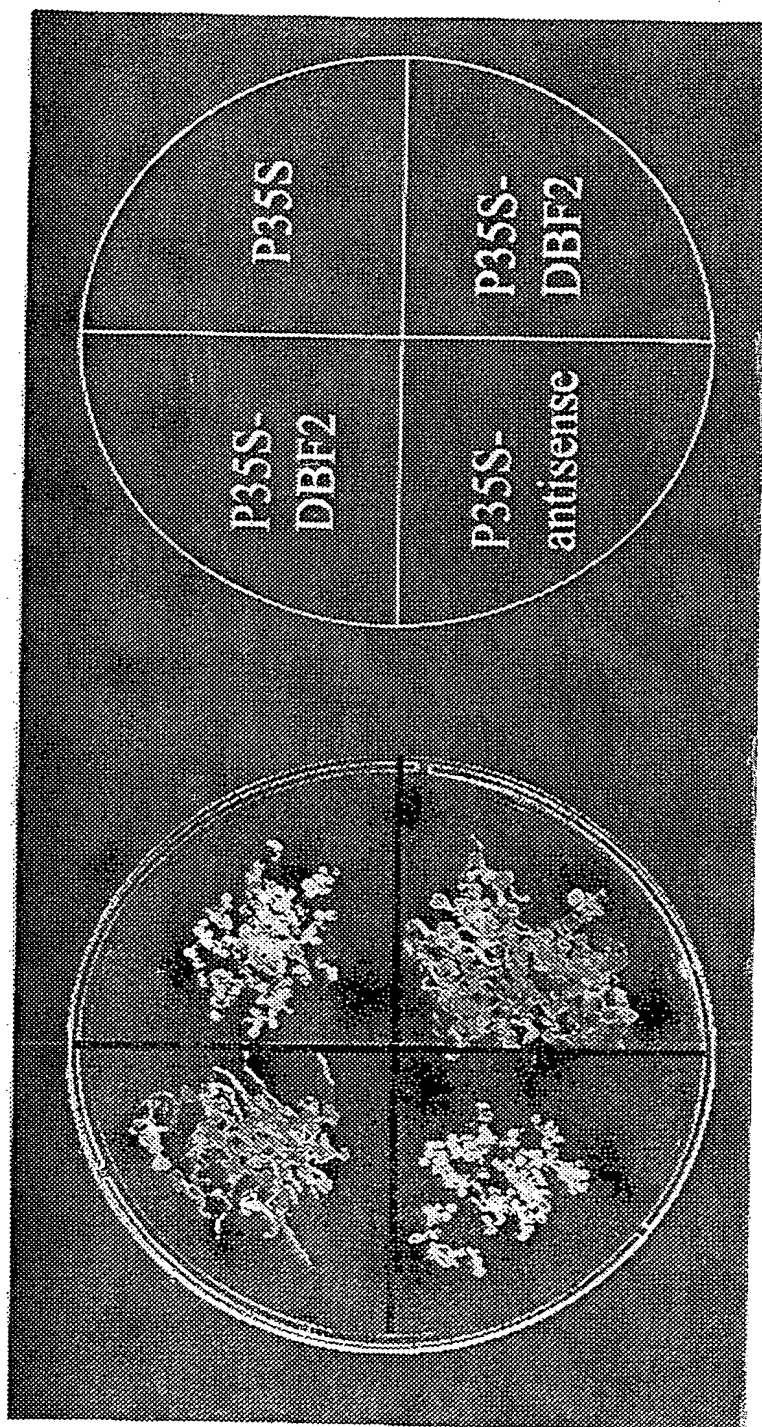


FIGURE 6

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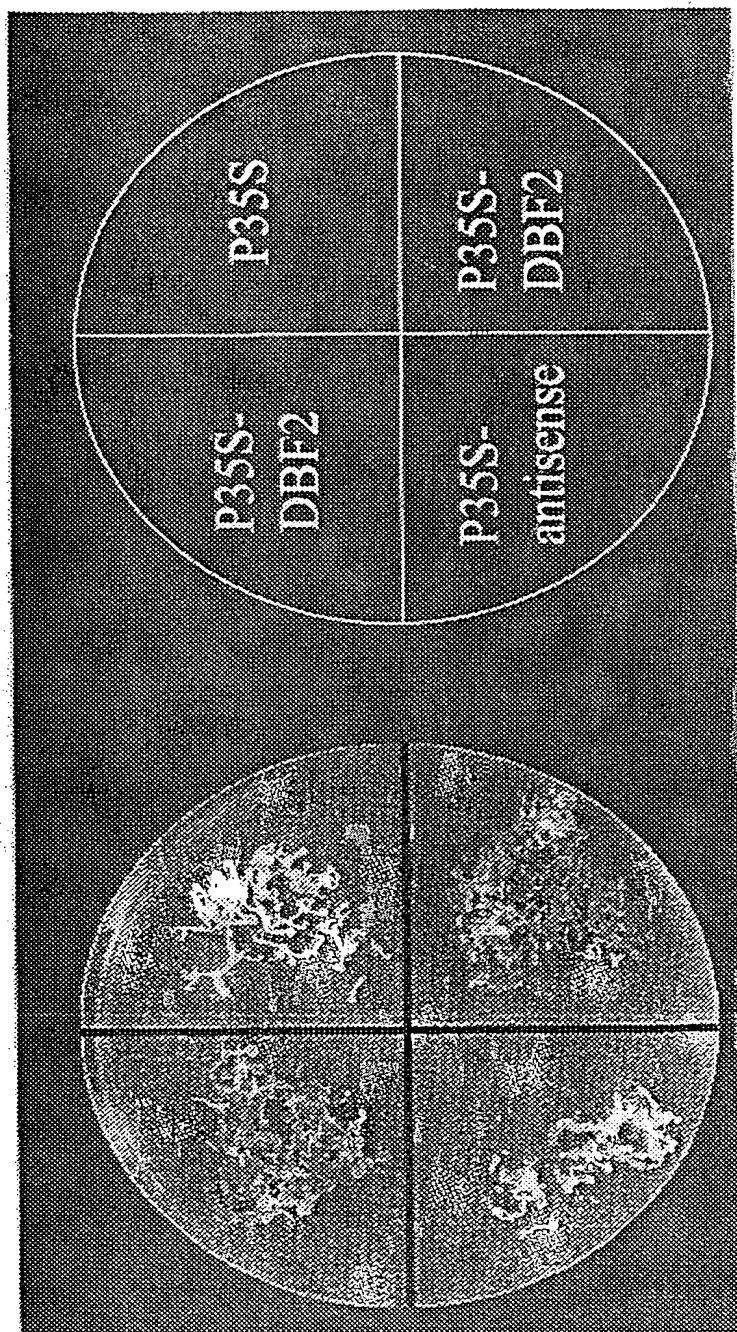


FIGURE 7

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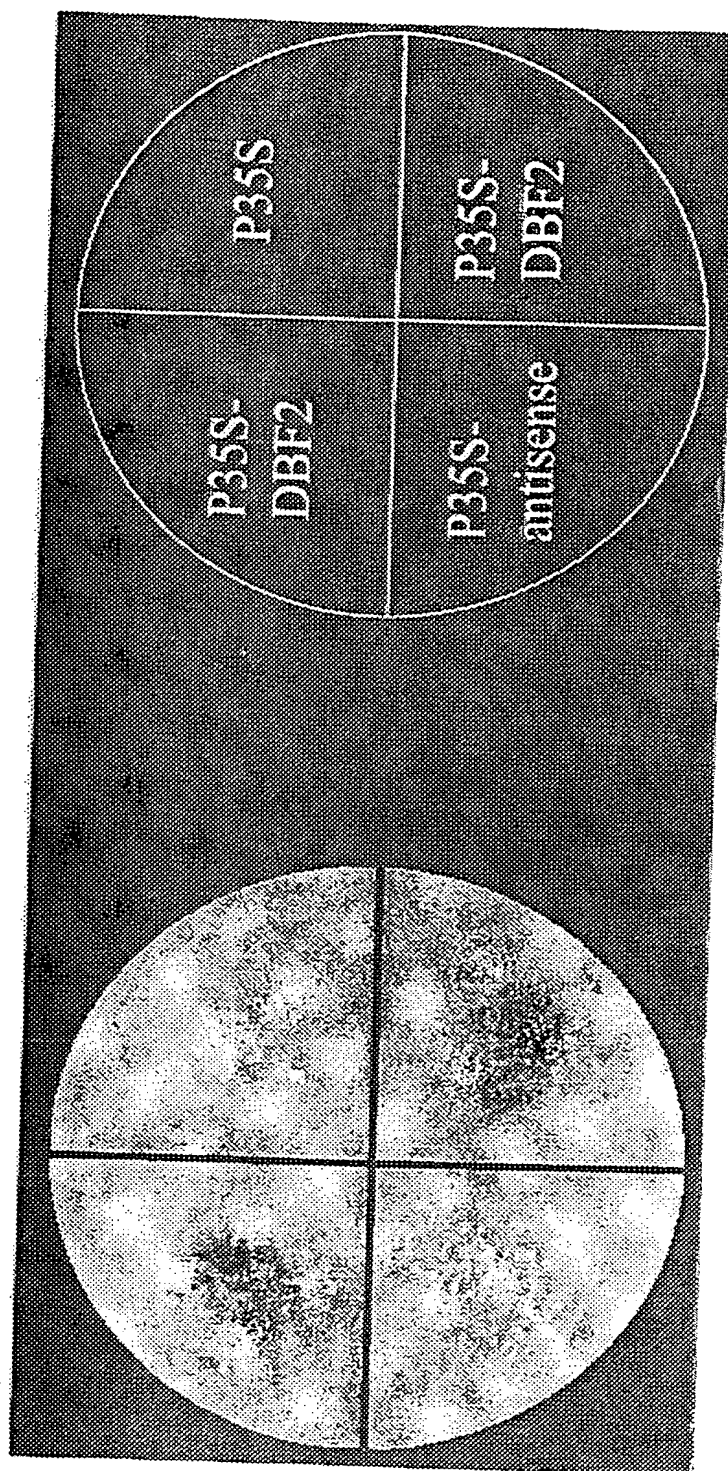


FIGURE 8

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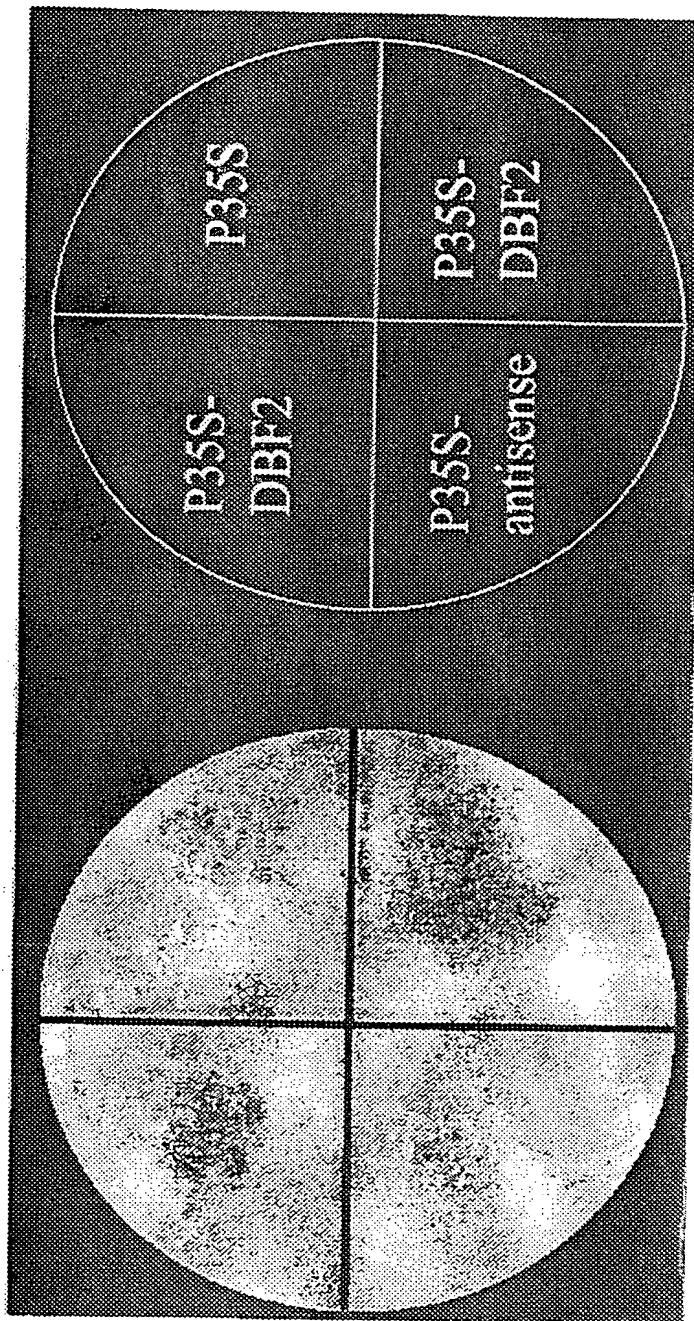


FIGURE 9

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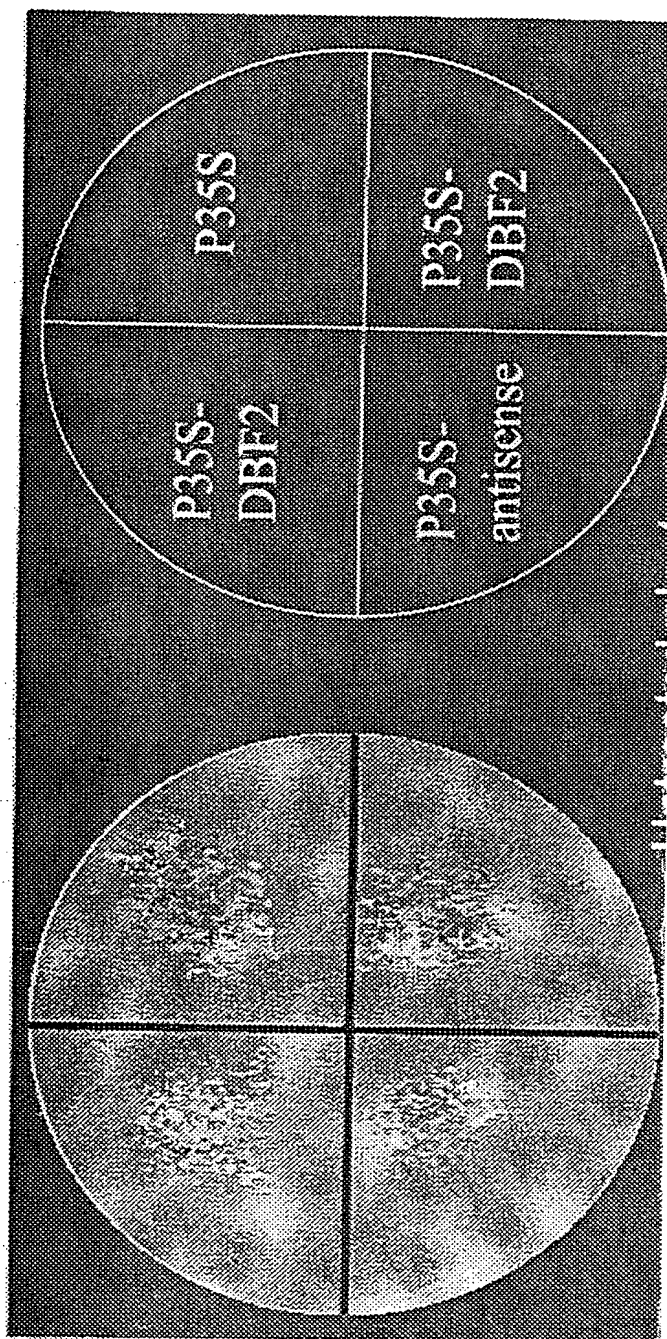


FIGURE 10

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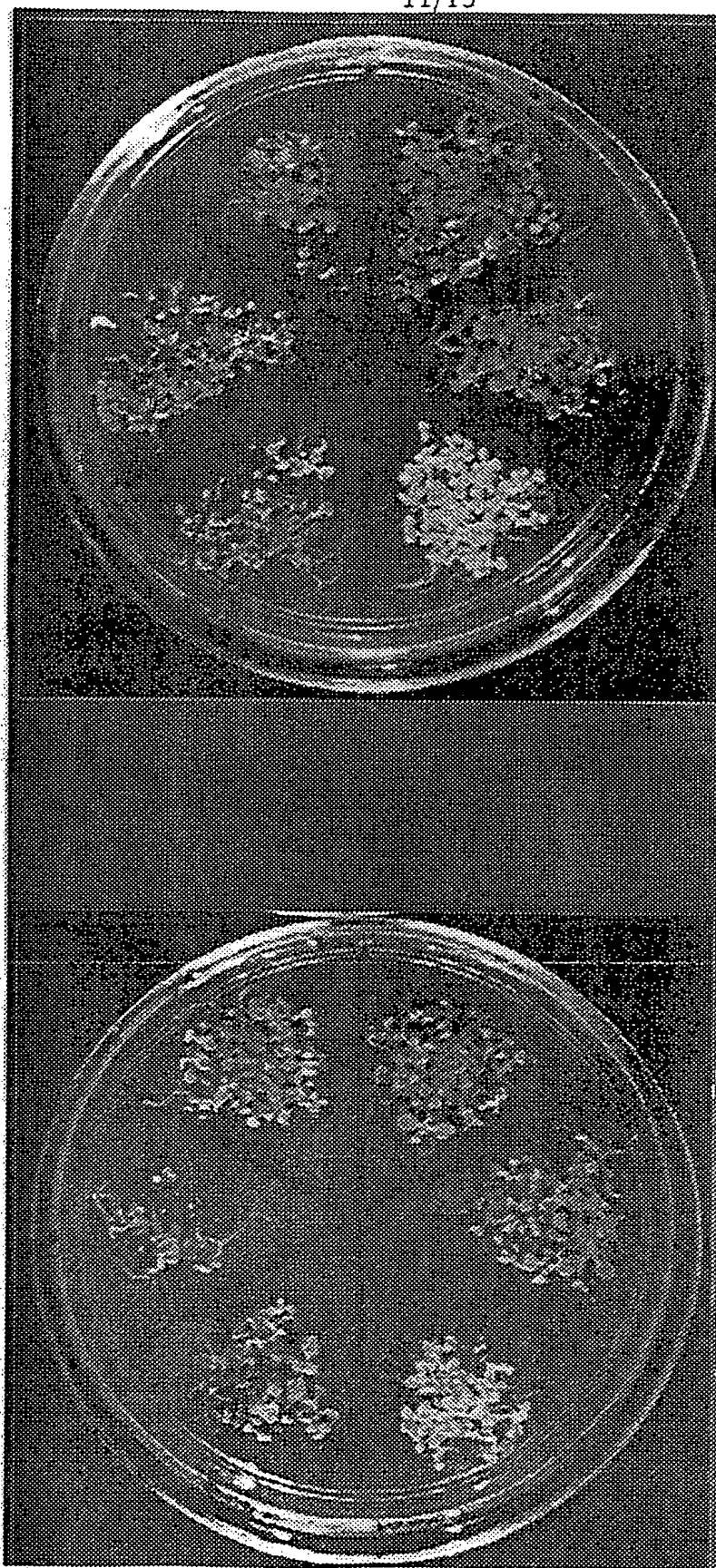


FIGURE 11

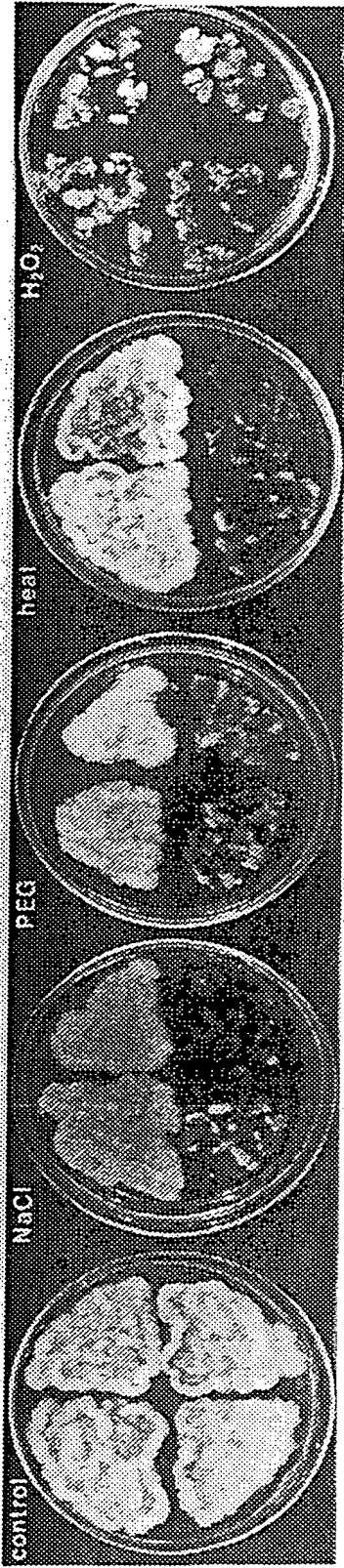


FIGURE 12A

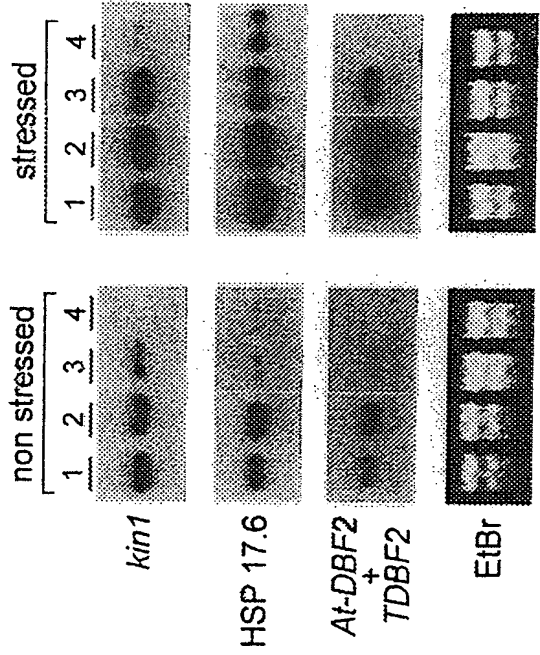


FIGURE 12c

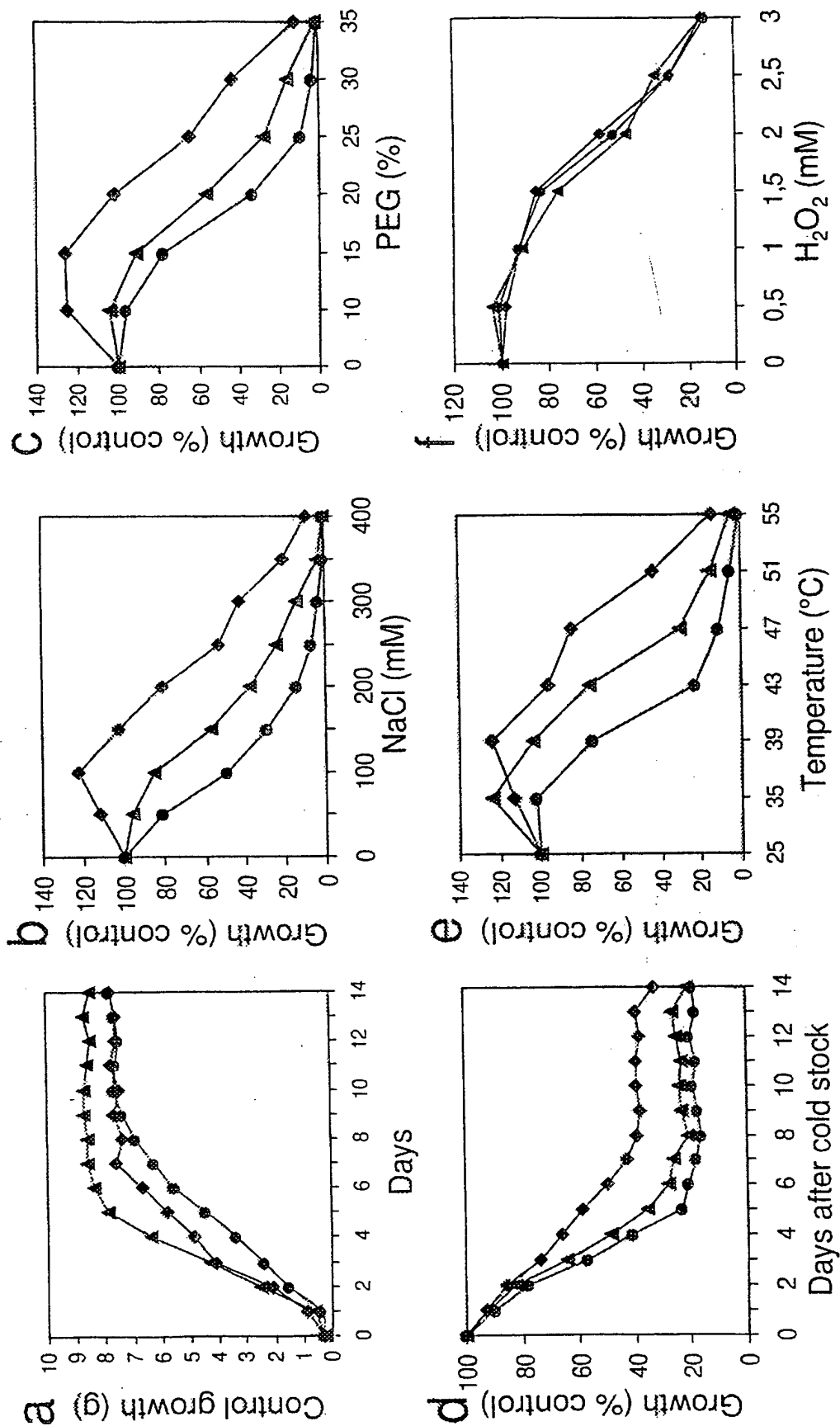


FIGURE 12B

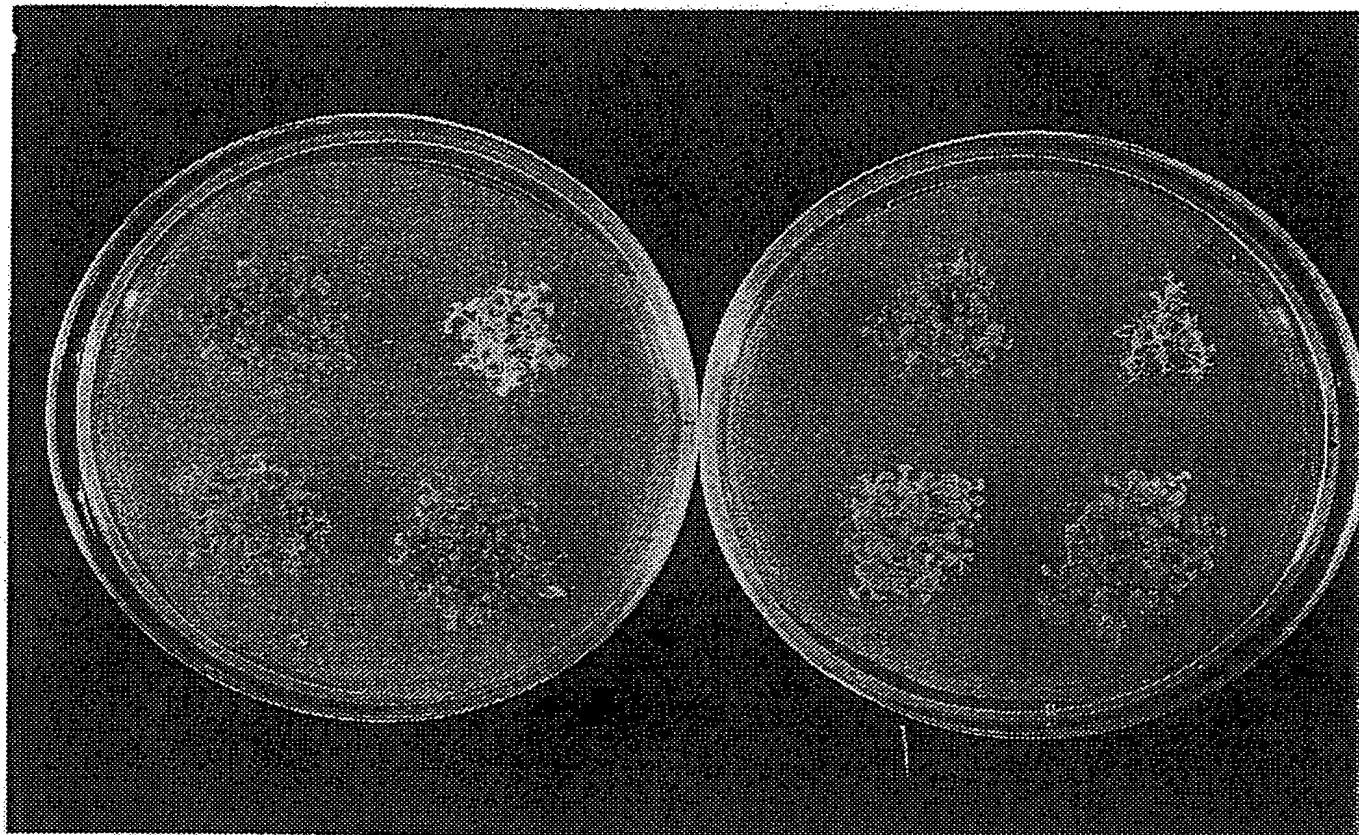


FIGURE 13

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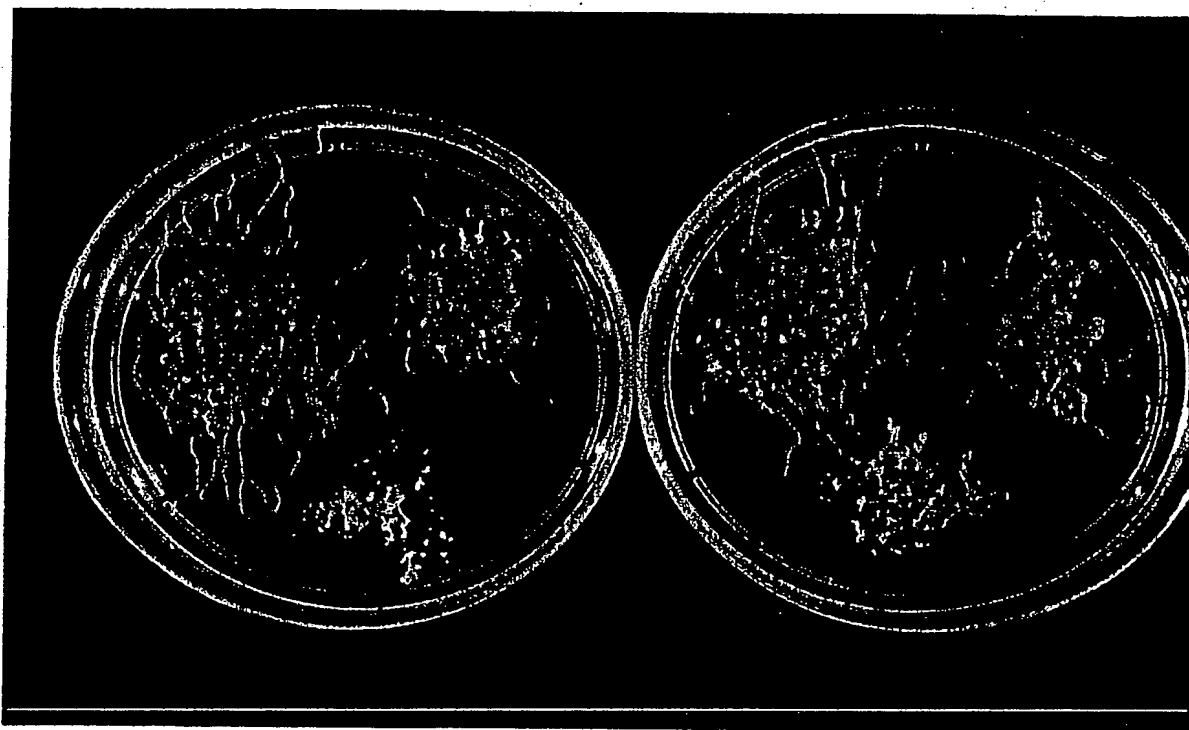


FIGURE 14

SEQUENCE LISTING

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<140>

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Phe Pro Asn Gln Asn Leu Thr Lys Arg Arg Thr Arg Pro Ala Gly Ile
              25              30              35

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Asn Asp Ser Pro Ser Pro Val Lys Cys Phe Phe Phe Pro Tyr Glu Asp
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Ser Asn Ser Pro Pro Val Ser Pro Ala Ile Phe Tyr Glu Arg Ala Thr
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Ser	Arg	Arg 115	Gln	Arg	Thr	Lys	Gln 120	Val	Leu	Glu	Tyr	Leu	Gln	Gln	Gln
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Ser 145	Tyr	Leu	Gln	Arg	Glu 150	His	Gln	Val	Leu	Ser 155	Lys	Arg	Arg	Leu	Lys 160
Pro	Lys	Asn	Arg	Asp 165	Phe	Glu	Met	Ile	Thr 170	Gln	Val	Gly	Gln	Gly 175	Gly
Tyr	Gly	His	Val 180	Tyr	Leu	Ala	Arg	Lys 185	Lys	Asp	Thr	Lys	Glu	Val	Cys
Ala	Leu	Lys 195	Ile	Leu	Asn	Lys	Lys 200	Leu	Gly	Phe	Lys	Leu	Asn	Gly	Thr
Cys	His 210	Val	Leu	Thr	Glu	Arg 215	Gln	Ser	Leu	Thr	Thr 220	Thr	Arg	Ser	Glu
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Met	Ala	Ile	Glu	Ser 245	Glu	Leu	Gly	Gly	Asp 250	Phe	Arg	Thr	Glu	Ser 255	Ile

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 Ser Trp Lys Gln Thr Leu Asn Arg Ala Arg His Glu Asp Gly Arg Ala
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 Leu Ser Thr Arg Thr Arg Ser Phe Glu His Glu Val Lys Met Ser Tyr
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 Phe Ala Asp Ile Leu Phe Lys Ala Leu Arg Ser Ile Ile Pro Pro Phe
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 Thr Pro Gln Leu Asp Ser Glu Thr Asp Ala Gly Tyr Phe Asp Asp Phe
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 Trp Asn Glu Ala Asp Ile Ala Lys Tyr Ala Asp Val Phe Asn Ser Gln
 465 470 475 480
 Cys Cys Arg Thr Ala Leu Val Asp Asp Ser Ala Val Ser Ser Lys Leu
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Phe Pro Ile Phe Ser Ile Leu Glu Asp Met Leu Glu Ala Pro Glu Glu
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Gln Thr Glu Lys Thr Arg Asn Asn Pro Ser Arg Ala Tyr Met Arg Asp
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Ala Lys Ala Met Ala Ala Thr Pro Ala Asp Val Ile Glu His Pro Asp
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gcg tac gtt ttc gcc gtg gac atg cct gga atc aaa gga gat gag att 306
Ala Tyr Val Phe Ala Val Asp Met Pro Gly Ile Lys Gly Asp Glu Ile
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Gln Val Gln Ile Glu Asn Glu Asn Val Leu Val Val Ser Gly Lys Arg
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Gln Arg Asp Asn Lys Glu Asn Glu Gly Val Lys Phe Val Arg Met Glu
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                               105                               110                               115

gat ttg gag aag atc tct gcg gct tgt aat gac ggt gtg ttg aaa gtg 498
Asp Leu Glu Lys Ile Ser Ala Ala Cys Asn Asp Gly Val Leu Lys Val
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act att ccg aaa ctt cct cct cct gag cca aag aaa cca aag act ata 546
Thr Ile Pro Lys Leu Pro Pro Pro Glu Pro Lys Lys Pro Lys Thr Ile
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Gln Val Gln Val Ala
                               155

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 35 40 45
 Asp Val Ile Glu His Pro Asp Ala Tyr Val Phe Ala Val Asp Met Pro
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 Gly Ile Lys Gly Asp Glu Ile Gln Val Gln Ile Glu Asn Glu Asn Val
 65 70 75 80
 Leu Val Val Ser Gly Lys Arg Gln Arg Asp Asn Lys Glu Asn Glu Gly
 85 90 95
 Val Lys Phe Val Arg Met Glu Arg Arg Met Gly Lys Phe Met Arg Lys
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 Phe Gln Leu Pro Asp Asn Ala Asp Leu Glu Lys Ile Ser Ala Ala Cys
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 ttccaatcat cc atg agt ccg gac aat aaa ctg ctt ccg aag cgg atc atc 171
 Met Ser Pro Asp Asn Lys Leu Leu Pro Lys Arg Ile Ile
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ctt gta cgg cac ggt gaa tcg gaa ggg aat ctc gac acg gcg gcg tat	219
Leu Val Arg His Gly Glu Ser Glu Gly Asn Leu Asp Thr Ala Ala Tyr	
15 20 25	
aca acg acg ccg gat cat aag atc cag tta acg gat tcc ggt ttg ctt	267
Thr Thr Thr Pro Asp His Lys Ile Gln Leu Thr Asp Ser Gly Leu Leu	
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Gln Ala Gln Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn	
50 55 60	
cct tct tca ccg gag tgg cgt gtg tac ttc tac gtt tcg ccg tac gat	363
Pro Ser Ser Pro Glu Trp Arg Val Tyr Phe Tyr Val Ser Pro Tyr Asp	
65 70 75	
cgg act cga tct acg ctc cgg gag atc gga cgg tcg ttc tcg cgt cgc	411
Arg Thr Arg Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg	
80 85 90	
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Arg Val Ile Gly Val Arg Glu Glu Cys Arg Ile Arg Glu Gln Asp Phe	
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Gly Asn Phe Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg	
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Glu Arg Phe Gly Arg Phe Phe Tyr Arg Phe Pro Glu Gly Glu Ser Ala	
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Asp Ile Asp Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn	
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Phe Val Ile Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys	
175 180 185	
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Trp Phe Lys Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly	
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Leu Ala Ile His His Thr Glu Glu Glu Leu Ala Thr Trp Gly Leu Ser	
225 230 235	
cca gag atg att gca gat caa aag tgg cgg gct aac gcg cat aaa ggc	891

Pro Glu Met Ile Ala Asp Gln Lys Trp Arg Ala Asn Ala His Lys Gly
 240 245 250

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 270 275 280 285

gaa gaa gaa gaa gaa gaa gag ggg aaa agg gta aat ctg cta acg agt 1035
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 305 310 315

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Glu Ala Gly Ala Arg Leu His Ala Leu Ile Ser Ser Asn Pro Ser Ser
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Ser Thr Leu Arg Glu Ile Gly Arg Ser Phe Ser Arg Arg Arg Val Ile
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Gln Val Lys Glu Arg Met Arg Ala Thr Lys Lys Val Arg Glu Arg Phe
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 Met Asn Arg Leu His Ile Asn Pro Ser His Glu Leu Asn Phe Val Ile
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 Val Ser His Gly Leu Thr Ser Arg Val Phe Leu Met Lys Trp Phe Lys
 180 185 190
 Trp Ser Val Glu Gln Phe Glu Gly Leu Asn Asn Pro Gly Asn Ser Glu
 195 200 205
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 210 215 220
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 225 230 235 240
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 Glu Asp Cys Lys Trp Tyr Phe Gly Asp Phe Phe Asp His Met Ala Asp
 260 265 270
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 Val Ala Ile Ile Thr Gly Gly Ala Arg Gly Ile Gly Ala Ala Thr Ala
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Arg Leu Phe Thr Glu Asn Gly Ala Tyr Val Ile Val Ala Asp Ile Leu	
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Asp Asn Glu Gly Ile Leu Val Ala Glu Ser Ile Gly Gly Cys Tyr Val	
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His Cys Asp Val Ser Lys Glu Ala Asp Val Glu Ala Ala Val Glu Leu	
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Ala Met Arg Arg Lys Gly Arg Leu Asp Val Met Phe Asn Asn Ala Gly	
80 85 90	
atg tcg ctt aac gaa ggt agt atc atg ggg atg gac gtg gac atg gtt	339
Met Ser Leu Asn Glu Gly Ser Ile Met Gly Met Asp Val Asp Met Val	
95 100 105	
aac aaa ctt gtc tcg gtt aat gtc aat ggt gtt ttg cat ggt atc aaa	387
Asn Lys Leu Val Ser Val Asn Val Asn Gly Val Leu His Gly Ile Lys	
110 115 120	
cat gcc gct aag gcc atg atc aaa ggg gga cga gga ggc tcg ata ata	435
His Ala Ala Lys Ala Met Ile Lys Gly Gly Arg Gly Gly Ser Ile Ile	
125 130 135	
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Cys Thr Ser Ser Ser Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala	
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Tyr Thr Leu Ser Lys Gly Gly Ile Asn Gly Val Val Arg Thr Thr Glu	
160 165 170	
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Cys Glu Leu Gly Ser His Gly Ile Arg Val Asn Ser Ile Ser Pro His	
175 180 185	
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Ser Gly Leu Met Gly Gly Leu Gly Gly His Ala Tyr Thr Leu Ser Lys
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His Gly Ile Arg Val Asn Ser Ile Ser Pro His Gly Val Pro Thr Asp
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Ile Leu Val Asn Ala Tyr Arg Lys Phe Leu Asn Asn Asp Lys Leu Asn
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 gagaaagaca cgccacatgt ggtttttggt gtttttttcc ttagattaga agttattttg 354

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                ly Pro Val Leu
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      Gly Asn Phe Asp Leu Val Gly Asn Asn Thr Pro Val Phe
      135                      140

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Phe Ile Arg Asp Gly Ile Gln Phe Pro Asp Val Val His Ala Leu Lys
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cct aac cga aaa aca aac atc caa gag tac tgg agg att ctg gac tac      1712
Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
      160                      165                      170                      175

atg tcc cac ttg cct gag agt ttg ctc aca tgg tgc tgg atg ttt gat      1760
Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
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gat gtt ggt att cca caa gat tac agg cat atg gag ggt ttc ggt gtc      1808
Asp Val Gly Ile Pro Gln Asp Tyr Arg His Met Glu Gly Phe Gly Val
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cac acc tac act ctt att gcc aaa tct gga aaa gtt ctc ttt gtg aag      1856
His Thr Tyr Thr Leu Ile Ala Lys Ser Gly Lys Val Leu Phe Val Lys
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ttc cac tgg aaa cca act tgt ggg atc aag aat ctg act gat gaa gag      1904
Phe His Trp Lys Pro Thr Cys Gly Ile Lys Asn Leu Thr Asp Glu Glu
      225                      230                      235

gcc aag gtt gtt gga gga gcc aat cac agc cac gcc act aag gat ctc      1952
Ala Lys Val Val Gly Gly Ala Asn His Ser His Ala Thr Lys Asp Leu
      240                      245                      250                      255

cac gat gcc att gca tct ggc aac tac ccc gag tgg aaa ctt ttc atc      2000
His Asp Ala Ile Ala Ser Gly Asn Tyr Pro Glu Trp Lys Leu Phe Ile
      260                      265                      270

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Gln Thr Met Asp Pro Ala Asp Glu Asp Lys Phe Asp Phe Asp Pro Leu
      275                      280                      285

gat gtg acc aag atc tgg cct gag gat att ttg cct ctg caa ccg gtt      2096
Asp Val Thr Lys Ile Trp Pro Glu Asp Ile Leu Pro Leu Gln Pro Val
      290                      295                      300

ggt cgc ttg gtt ctg aac agg acc att gac aac ttc ttc aat gaa act      2144
Gly Arg Leu Val Leu Asn Arg Thr Ile Asp Asn Phe Phe Asn Glu Thr
      305                      310                      315

gag cag ctt gcg ttc aac ccg ggt ctt gtg gtt cct gga atc tac tac      2192
Glu Gln Leu Ala Phe Asn Pro Gly Leu Val Val Pro Gly Ile Tyr Tyr

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Ser Asp Asp Lys Leu Leu Gln Cys Arg Ile Phe Ala Tyr Gly Asp Thr	340	345	350	
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Gln Arg His Arg Leu Gly Pro Asn Tyr Leu Gln Leu Pro Val Asn Ala	355	360	365	
ccc aaa tgt gct cac cac aac aat cac cat gaa ggt ttt atg aac ttc				2336
Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe	370	375	380	
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Met His Arg Asp Glu Glu	385			
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			Ile	
			390	
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Asn Tyr Tyr Pro Ser Lys Phe Asp Pro Val Arg Cys Ala Glu Lys Val	395	400	405	
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Pro Thr Pro Thr Asn Ser Tyr Thr Gly Ile Arg Thr Lys	410	415		
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agaaaacctt ttaattgcta atgttgtag tgc gtc atc aag aaa gag aac aac				2652
		Cys Val Ile Lys Lys	Glu Asn Asn	
		420	425	
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Phe Lys Gln Ala Gly Asp Arg Tyr Arg Ser Trp Ala Pro Asp Arg Gln	430	435	440	
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Asp Arg Phe Val Lys Arg Trp Val Glu Ile Leu Ser Glu Pro Arg Leu	445	450	455	
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Thr His Glu Ile Arg Gly Ile Trp Thr Ser Tyr Trp Leu Lys	460	465	470	
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Lys Leu Ala Ser Arg Leu Asn Val Arg Pro Ser Ile	485	490		

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 Gln Thr Pro Val Ile Val Arg Phe Ser Thr Val Val His Gly Arg Ala
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 Ser Pro Glu Thr Met Arg Asp Ile Arg Gly Phe Ala Val Lys Phe Tyr
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 Pro Asn Arg Lys Thr Asn Ile Gln Glu Tyr Trp Arg Ile Leu Asp Tyr
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 Met Ser His Leu Pro Glu Ser Leu Leu Thr Trp Cys Trp Met Phe Asp
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 Pro Lys Cys Ala His His Asn Asn His His Glu Gly Phe Met Asn Phe
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 Gln Ala Glu Ile Asn Gln Leu Leu Ser Leu Ile Ile Asn Thr Phe Tyr
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 gac aag cct aat aag acg ctc tca att att gac agt ggt att ggc atg 652
 Asp Lys Pro Asn Lys Thr Leu Ser Ile Ile Asp Ser Gly Ile Gly Met
 75 80 85 90
 acc aaa gca ggtaacgaat caatgcctaa taatctctcg ttggtgagat 701
 Thr Lys Ala
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Asn	Leu	Gly	Thr	Ile	Ala	Arg	Ser	Gly	Thr	Lys	Glu	Phe	Met	Glu	Ala					
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Leu	Gln	Ala	Gly	Ala	Asp	Val	Ser	Met	Ile	Gly	Gln	Phe	Gly	Val	Gly					
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ctc	atc	aac	aag	cag	aaa	ccg	atc	tgg	ttg	agg	aag	cca	gaa	gag	atc	1395				
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 Ser Lys Thr Gly Gly Pro Asn Gly Ser Ile Arg Asn Glu Glu Glu His
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 Thr His Gly Ala Asn Ser Gly Leu Lys Ile Ala Leu Asp Leu Cys Glu
 65 70 75 80
 Gly Val Lys Ala Lys His Pro Lys Ile Thr Tyr Ala Asp Leu Tyr Gln
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 Leu Ala Gly Val Val Ala Val Glu Val Thr Gly Gly Pro Asp Ile Val
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 Phe Val Pro Gly Arg Lys Asp Ser Asn Val Cys Pro Lys Glu Gly Arg
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 Leu Pro Asp Ala Lys Gln Gly Phe Gln His Leu Arg Asp Val Phe Tyr
 130 135 140

37

Arg Met Gly Leu Ser Asp Lys Asp Ile Val Ala Leu Ser Gly Gly His
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 Thr Leu Gly Arg Ala His Pro Glu Arg Ser Gly Phe Asp Gly Pro Trp
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 180 185 190
 Leu Lys Gly Glu Ser Glu Gly Leu Leu Lys Leu Pro Thr Asp Lys Thr
 195 200 205
 Leu Leu Glu Asp Pro Glu Phe Arg Arg Leu Val Glu Leu Tyr Ala Asp
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 Glu Asp Ala Phe Phe Arg Asp Tyr Ala Glu Ser His Lys Lys Leu Ser
 225 230 235 240
 Glu Leu Gly Phe Asn Pro Asn Ser Ser Ala Gly Lys Ala Val Ala Asp
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38

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 Ser Glu Leu Arg Pro His Ala Gly Gly Asp Tyr Ser Ile Ala Val Val
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 Gln Ala Asn Ser Arg Leu Glu Asp Gln Ser Gln Val Phe Thr Ser Ser
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 Ser Ala Thr Tyr Val Gly Val Tyr Asp Gly His Gly Gly Pro Glu Ala
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Val Glu Ile Val Leu Lys His Pro Arg Thr			
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Tyr Leu Asp Gln Asn Lys Thr Ser Ser Ser Asn Ser Lys Leu Val Lys			
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caa gga ggt atc acc gct cca ccg gat atc tac tca tta cac tct gat	1814		
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Tyr Asp Gly His Gly Gly Pro Glu Ala Ser Arg Phe Val Asn Arg His
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Leu Phe Pro Tyr Met His Lys Phe Ala Arg Glu His Gly Gly Leu Ser
 85 90 95

Val Asp Val Ile Lys Lys Ala Phe Lys Glu Thr Glu Glu Glu Phe Cys
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Gly Met Val Lys Arg Ser Leu Pro Met Lys Pro Gln Met Ala Thr Val
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Gly Ser Cys Cys Leu Val Gly Ala Ile Ser Asn Asp Thr Leu Tyr Val
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Asp Asp Ser Gln Ile Val Leu Tyr Thr Arg Gly Val Trp Arg Ile Lys
 195 200 205

Gly Ile Ile Gln Val Ser Arg Ser Ile Gly Asp Val Tyr Leu Lys Lys
 210 215 220

Pro Glu Tyr Tyr Arg Asp Pro Ile Phe Gln Arg His Gly Asn Pro Ile
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	290					295				300					
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Lys	Gly	Ile	Arg	Arg	His	Phe	His	Asp	Asp	Ile	Ser	Val	Ile	Val	Val
				325					330					335	
Tyr	Leu	Asp	Gln	Asn	Lys	Thr	Ser	Ser	Ser	Asn	Ser	Lys	Leu	Val	Lys
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Gln	Gly	Gly	Ile	Thr	Ala	Pro	Pro	Asp	Ile	Tyr	Ser	Leu	His	Ser	Asp
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Lys Glu Val Ser Arg Ser Thr Phe Ser Ala Val Phe Ser Lys Pro Lys
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Gly Asn Asp Lys A
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 1 5 10
 ggc act cgc ttg aga cca ttg act ctc agt ttc cca aag ccc ctt gtt 99
 Gly Thr Arg Leu Arg Pro Leu Thr Leu Ser Phe Pro Lys Pro Leu Val
 15 20 25
 gat ttt gct aat aaa ccc atg atc ctt cat cag ata gag gct ctt aag 147
 Asp Phe Ala Asn Lys Pro Met Ile Leu His Gln Ile Glu Ala Leu Lys
 30 35 40
 gca gtt gga gtt gat gaa gtg gtt ttg gcc atc aat tat cag cca gag 195
 Ala Val Gly Val Asp Glu Val Val Leu Ala Ile Asn Tyr Gln Pro Glu
 45 50 55
 gtg atg ctg aac ttc ttg aag gac ttt gag acc aag ctg gaa atc aaa 243
 Val Met Leu Asn Phe Leu Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys
 60 65 70
 atc act tgc tca caa gag acc gag cca cta ggt acc gct ggt cct ctg 291
 Ile Thr Cys Ser Gln Glu Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu
 75 80 85 90
 gct cta gcg aga gac aaa ttg ctt gat gga tct gga gag ccc ttc ttt 339
 Ala Leu Ala Arg Asp Lys Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe

95										100					105					
gtt	ctt	aac	agt	gat	gtg	att	agt	gag	tac	cct	ctt	aaa	gaa	atg	ctt	387				
Val	Leu	Asn	Ser	Asp	Val	Ile	Ser	Glu	Tyr	Pro	Leu	Lys	Glu	Met	Leu					
			110					115					120							
gag	ttt	cac	aaa	tct	cac	ggg	ggg	gaa	gcc	tcc	ata	atg	gta	aca	aag	435				
Glu	Phe	His	Lys	Ser	His	Gly	Gly	Glu	Ala	Ser	Ile	Met	Val	Thr	Lys					
		125					130					135								
gtg	gat	gaa	ccg	tcg	aaa	tat	gga	gtg	gtt	gtt	atg	gaa	gaa	agc	act	483				
Val	Asp	Glu	Pro	Ser	Lys	Tyr	Gly	Val	Val	Val	Met	Glu	Glu	Ser	Thr					
	140					145					150									
gga	aga	gtg	gag	aag	ttt	gtg	gaa	aag	cca	aaa	ctg	tat	gta	ggg	aac	531				
Gly	Arg	Val	Glu	Lys	Phe	Val	Glu	Lys	Pro	Lys	Leu	Tyr	Val	Gly	Asn					
155					160					165					170					
aag	atc	aac	gct	ggg	att	tat	ctt	ctg	aac	cca	tct	gtt	ctt	gat	aag	579				
Lys	Ile	Asn	Ala	Gly	Ile	Tyr	Leu	Leu	Asn	Pro	Ser	Val	Leu	Asp	Lys					
			175						180					185						
att	gag	cta	aga	ccg	act	tca	atc	gaa	aaa	gag	act	ttc	cct	aag	att	627				
Ile	Glu	Leu	Arg	Pro	Thr	Ser	Ile	Glu	Lys	Glu	Thr	Phe	Pro	Lys	Ile					
			190					195					200							
gca	gca	gcg	caa	ggg	ctc	tat	gct	atg	gtg	cta	cca	ggg	ttt	tgg	atg	675				
Ala	Ala	Ala	Gln	Gly	Leu	Tyr	Ala	Met	Val	Leu	Pro	Gly	Phe	Trp	Met					
		205					210					215								
gac	att	ggg	caa	ccc	cgt	gac	tac	ata	acg	ggg	ttg	aga	ctc	tac	tta	723				
Asp	Ile	Gly	Gln	Pro	Arg	Asp	Tyr	Ile	Thr	Gly	Leu	Arg	Leu	Tyr	Leu					
	220					225					230									
gac	tcc	ctt	agg	aag	aaa	tct	cct	gcc	aaa	tta	acc	agt	ggg	cca	cac	771				
Asp	Ser	Leu	Arg	Lys	Lys	Ser	Pro	Ala	Lys	Leu	Thr	Ser	Gly	Pro	His					
235					240					245					250					
ata	gtt	ggg	aat	gtt	ctt	gtt	gac	gaa	acc	gct	aca	att	ggg	gaa	gga	819				
Ile	Val	Gly	Asn	Val	Leu	Val	Asp	Glu	Thr	Ala	Thr	Ile	Gly	Glu	Gly					
			255					260						265						
tgt	ttg	att	gga	cca	gac	gtt	gcc	att	ggg	cca	ggc	tgc	att	gtt	gag	867				
Cys	Leu	Ile	Gly	Pro	Asp	Val	Ala	Ile	Gly	Pro	Gly	Cys	Ile	Val	Glu					
			270				275						280							
tca	gga	gtc	aga	ctc	tcc	cga	tgc	acg	gtc	atg	cgt	gga	gtc	cgc	atc	915				
Ser	Gly	Val	Arg	Leu	Ser	Arg	Cys	Thr	Val	Met	Arg	Gly	Val	Arg	Ile					
		285					290					295								
aag	aag	cat	gcg	tgt	atc	tcg	agc	agt	atc	atc	ggg	tgg	cac	tca	acg	963				
Lys	Lys	His	Ala	Cys	Ile	Ser	Ser	Ser	Ile	Ile	Gly	Trp	His	Ser	Thr					
		300				305					310									
gtt	ggg	caa	tgg	gcc	agg	atc	gag	aac	atg	acg	atc	ctc	ggg	gag	gat	1011				
Val	Gly	Gln	Trp	Ala	Arg	Ile	Glu	Asn	Met	Thr	Ile	Leu	Gly	Glu	Asp					
315					320					325					330					

gtt cat gtg agc gat gag atc tat agc aat gga gga gtt gtt ttg cca 1059
 Val His Val Ser Asp Glu Ile Tyr Ser Asn Gly Gly Val Val Leu Pro
 335 340 345

cac aag gag atc aaa tca aac atc ttg aag cca gag ata gtg atg tga 1107
 His Lys Glu Ile Lys Ser Asn Ile Leu Lys Pro Glu Ile Val Met
 350 355 360

aa 1109

<210> 24

<211> 361

<212> PRT

<213> Arabidopsis thaliana

<400> 24

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Met Ile Leu His Gln Ile Glu Ala Leu Lys Ala Val Gly Val Asp Glu
 35 40 45

Val Val Leu Ala Ile Asn Tyr Gln Pro Glu Val Met Leu Asn Phe Leu
 50 55 60

Lys Asp Phe Glu Thr Lys Leu Glu Ile Lys Ile Thr Cys Ser Gln Glu
 65 70 75 80

Thr Glu Pro Leu Gly Thr Ala Gly Pro Leu Ala Leu Ala Arg Asp Lys
 85 90 95

Leu Leu Asp Gly Ser Gly Glu Pro Phe Phe Val Leu Asn Ser Asp Val
 100 105 110

Ile Ser Glu Tyr Pro Leu Lys Glu Met Leu Glu Phe His Lys Ser His
 115 120 125

Gly Gly Glu Ala Ser Ile Met Val Thr Lys Val Asp Glu Pro Ser Lys
 130 135 140

Tyr Gly Val Val Val Met Glu Glu Ser Thr Gly Arg Val Glu Lys Phe
 145 150 155 160

Val Glu Lys Pro Lys Leu Tyr Val Gly Asn Lys Ile Asn Ala Gly Ile
 165 170 175

Tyr Leu Leu Asn Pro Ser Val Leu Asp Lys Ile Glu Leu Arg Pro Thr
 180 185 190

Ser Ile Glu Lys Glu Thr Phe Pro Lys Ile Ala Ala Ala Gln Gly Leu
 195 200 205

Tyr Ala Met Val Leu Pro Gly Phe Trp Met Asp Ile Gly Gln Pro Arg
 210 215 220
 Asp Tyr Ile Thr Gly Leu Arg Leu Tyr Leu Asp Ser Leu Arg Lys Lys
 225 230 235 240
 Ser Pro Ala Lys Leu Thr Ser Gly Pro His Ile Val Gly Asn Val Leu
 245 250 255
 Val Asp Glu Thr Ala Thr Ile Gly Glu Gly Cys Leu Ile Gly Pro Asp
 260 265 270
 Val Ala Ile Gly Pro Gly Cys Ile Val Glu Ser Gly Val Arg Leu Ser
 275 280 285
 Arg Cys Thr Val Met Arg Gly Val Arg Ile Lys Lys His Ala Cys Ile
 290 295 300
 Ser Ser Ser Ile Ile Gly Trp His Ser Thr Val Gly Gln Trp Ala Arg
 305 310 315 320
 Ile Glu Asn Met Thr Ile Leu Gly Glu Asp Val His Val Ser Asp Glu
 325 330 335
 Ile Tyr Ser Asn Gly Gly Val Val Leu Pro His Lys Glu Ile Lys Ser
 340 345 350
 Asn Ile Leu Lys Pro Glu Ile Val Met
 355 360

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 <213> Arabidopsis thaliana

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 1 5 10
 cct tat cga acc aac tct tct ttc ggc tca aag tca tcg ctt ctc ttt 98
 Pro Tyr Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe
 15 20 25 30
 cgg tct cca tcc tcc tcc tcc tca gtc tct atg acg aca acg cgt gga 146
 Arg Ser Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly
 35 40 45
 aac gtg gct gtg gcg gct gct gct aca tcc act gag gcg cta aga aaa 194
 Asn Val Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys
 50 55 60

gga ata gcg gag ttc tac aat gaa act tcg ggt ttg tgg gaa gag att	242
Gly Ile Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile	
65 70 75	
tgg gga gat cat atg cat cat ggc ttt tat gac cct gat tct tct gtt	290
Trp Gly Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val	
80 85 90	
caa ctt tct gat tct ggt cac aag gaa gct cag atc cgt atg att gaa	338
Gln Leu Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu	
95 100 105 110	
gag tct ctc cgt ttc gcc ggt gtt act gat gaa gag gag gag aaa aag	386
Glu Ser Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys	
115 120 125	
ata aag aaa gta gtg gat gtt ggg tgt ggg att gga gga agc tca aga	434
Ile Lys Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg	
130 135 140	
tat ctt gcc tct aaa ttt gga gct gaa tgc att ggc att act ctc agc	482
Tyr Leu Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser	
145 150 155	
cct gtt cag gcc aag aga gcc aat gat ctc gcg gct gct caa tca ctc	530
Pro Val Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu	
160 165 170	
tct cat aag gct tcc ttc caa gtt gcg gat gcg ttg gat cag cca ttc	578
Ser His Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe	
175 180 185 190	
gaa gat gga aaa ttc gat cta gtg tgg tcg atg gag agt ggt gag cat	626
Glu Asp Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His	
195 200 205	
atg cct gac aag gcc aag ttt gta aaa gag ttg gta cgt gtg gcg gct	674
Met Pro Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala	
210 215 220	
cca gga ggt agg ata ata ata gtg aca tgg tgc cat aga aat cta tct	722
Pro Gly Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser	
225 230 235	
gcg ggg gag gaa gct ttg cag ccg tgg gag caa aac atc ttg gac aaa	770
Ala Gly Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys	
240 245 250	
atc tgt aag acg ttc tat ctc ccg gct tgg tgc tcc acc gat gat tat	818
Ile Cys Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr	
255 260 265 270	
gtc aac ttg ctt caa tcc cat tct ctc cag gat att aag tgt gcg gat	866
Val Asn Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp	
275 280 285	

tgg tca gag aac gta gct cct ttc tgg cct gcg gtt ata cgg act gca 914
 Trp Ser Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala
 290 295 300
 tta aca tgg aag ggc ctt gtg tct ctg ctt cgt agt ggt atg aaa agt 962
 Leu Thr Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser
 305 310 315
 att aaa gga gca ttg aca atg cca ttg atg att gaa ggt tac aag aaa 1010
 Ile Lys Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys
 320 325 330
 ggt gtc att aag ttt ggt atc atc act tgc cag aag cca ctc taa 1055
 Gly Val Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
 335 340 345
 gtctaaagct atacta 1071

<210> 26
 <211> 348
 <212> PRT
 <213> Arabidopsis thaliana

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 Arg Thr Asn Ser Ser Phe Gly Ser Lys Ser Ser Leu Leu Phe Arg Ser
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 Pro Ser Ser Ser Ser Ser Val Ser Met Thr Thr Thr Arg Gly Asn Val
 35 40 45
 Ala Val Ala Ala Ala Ala Thr Ser Thr Glu Ala Leu Arg Lys Gly Ile
 50 55 60
 Ala Glu Phe Tyr Asn Glu Thr Ser Gly Leu Trp Glu Glu Ile Trp Gly
 65 70 75 80
 Asp His Met His His Gly Phe Tyr Asp Pro Asp Ser Ser Val Gln Leu
 85 90 95
 Ser Asp Ser Gly His Lys Glu Ala Gln Ile Arg Met Ile Glu Glu Ser
 100 105 110
 Leu Arg Phe Ala Gly Val Thr Asp Glu Glu Glu Glu Lys Lys Ile Lys
 115 120 125
 Lys Val Val Asp Val Gly Cys Gly Ile Gly Gly Ser Ser Arg Tyr Leu
 130 135 140
 Ala Ser Lys Phe Gly Ala Glu Cys Ile Gly Ile Thr Leu Ser Pro Val
 145 150 155 160
 Gln Ala Lys Arg Ala Asn Asp Leu Ala Ala Ala Gln Ser Leu Ser His
 165 170 175

Lys Ala Ser Phe Gln Val Ala Asp Ala Leu Asp Gln Pro Phe Glu Asp
 180 185 190
 Gly Lys Phe Asp Leu Val Trp Ser Met Glu Ser Gly Glu His Met Pro
 195 200 205
 Asp Lys Ala Lys Phe Val Lys Glu Leu Val Arg Val Ala Ala Pro Gly
 210 215 220
 Gly Arg Ile Ile Ile Val Thr Trp Cys His Arg Asn Leu Ser Ala Gly
 225 230 235 240
 Glu Glu Ala Leu Gln Pro Trp Glu Gln Asn Ile Leu Asp Lys Ile Cys
 245 250 255
 Lys Thr Phe Tyr Leu Pro Ala Trp Cys Ser Thr Asp Asp Tyr Val Asn
 260 265 270
 Leu Leu Gln Ser His Ser Leu Gln Asp Ile Lys Cys Ala Asp Trp Ser
 275 280 285
 Glu Asn Val Ala Pro Phe Trp Pro Ala Val Ile Arg Thr Ala Leu Thr
 290 295 300
 Trp Lys Gly Leu Val Ser Leu Leu Arg Ser Gly Met Lys Ser Ile Lys
 305 310 315 320
 Gly Ala Leu Thr Met Pro Leu Met Ile Glu Gly Tyr Lys Lys Gly Val
 325 330 335
 Ile Lys Phe Gly Ile Ile Thr Cys Gln Lys Pro Leu
 340 345

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 <222> (3)..(752)

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 ctc gag atc gac gat gac cag aaa cta cgt gcg ttt tac gac aag aga 95
 Leu Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg
 20 25 30
 atc tct caa gaa gtc agt gga gat gct ttg ggc gag gag ttc aaa gga 143
 Ile Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly
 35 40 45

tac gtt ttc aag atc aag ggt ggt tgc gat aag caa ggt ttc cca atg 191
 Tyr Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met
 50 55 60

aag cag gga gtt ttg act cca ggc cgt gtt cgc ctt ttg ctt cac cga 239
 Lys Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg
 65 70 75

gga act cct tgc ttc aga gga cat gga agg aga act ggt gag agg aga 287
 Gly Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg
 80 85 90 95

aga aag tct gtt cgt ggt tgc att gtg agc cct gat ctc tct gtt ctg 335
 Arg Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu
 100 105 110

aac ctt gtc att gtg aag aag ggt gag aac gat ctt cct ggg ctt acc 383
 Asn Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr
 115 120 125

gat cat gag agc aag atg aga gga cca aag aga gcc tcc aag atc cgt 431
 Asp His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg
 130 135 140

aaa ctg ttt aac ctc aag aag gaa gat gat gtc agg acc tat gtc aac 479
 Lys Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn
 145 150 155

act tac cgc cgc aag ttc aca aac aag aag ggc aag gaa gtt agc aaa 527
 Thr Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys
 160 165 170 175

gcc cct aag atc cag agg ctt gtg acc cca ttg act ctt cag agg aag 575
 Ala Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys
 180 185 190

aga gct aga att gct gac aag aag aag aaa att gct aag gct aat tct 623
 Arg Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser
 195 200 205

gat gct gct gat tac cag aag ctt ctc gcc tcg agg ttg aag gaa cag 671
 Asp Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln
 210 215 220

cgt gac agg agg agt gag agt ttg gca aaa gag agg tcg aga ctc tct 719
 Arg Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser
 225 230 235

tct gct gct gcc aag ccc tct gtc aca gct taa aaaagcttga gattca 768
 Ser Ala Ala Ala Lys Pro Ser Val Thr Ala
 240 245 250

<210> 28

<211> 249

<212> PRT

<213> Arabidopsis thaliana

<400> 28

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Met Lys Phe Asn Val Ala Asn Pro Thr Thr Gly Cys Gln Lys Lys Leu
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Glu Ile Asp Asp Asp Gln Lys Leu Arg Ala Phe Tyr Asp Lys Arg Ile
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Ser Gln Glu Val Ser Gly Asp Ala Leu Gly Glu Glu Phe Lys Gly Tyr
      35           40           45

Val Phe Lys Ile Lys Gly Gly Cys Asp Lys Gln Gly Phe Pro Met Lys
      50           55           60

Gln Gly Val Leu Thr Pro Gly Arg Val Arg Leu Leu Leu His Arg Gly
      65           70           75           80

Thr Pro Cys Phe Arg Gly His Gly Arg Arg Thr Gly Glu Arg Arg Arg
      85           90           95

Lys Ser Val Arg Gly Cys Ile Val Ser Pro Asp Leu Ser Val Leu Asn
      100          105          110

Leu Val Ile Val Lys Lys Gly Glu Asn Asp Leu Pro Gly Leu Thr Asp
      115          120          125

His Glu Ser Lys Met Arg Gly Pro Lys Arg Ala Ser Lys Ile Arg Lys
      130          135          140

Leu Phe Asn Leu Lys Lys Glu Asp Asp Val Arg Thr Tyr Val Asn Thr
      145          150          155          160

Tyr Arg Arg Lys Phe Thr Asn Lys Lys Gly Lys Glu Val Ser Lys Ala
      165          170          175

Pro Lys Ile Gln Arg Leu Val Thr Pro Leu Thr Leu Gln Arg Lys Arg
      180          185          190

Ala Arg Ile Ala Asp Lys Lys Lys Lys Ile Ala Lys Ala Asn Ser Asp
      195          200          205

Ala Ala Asp Tyr Gln Lys Leu Leu Ala Ser Arg Leu Lys Glu Gln Arg
      210          215          220

Asp Arg Arg Ser Glu Ser Leu Ala Lys Glu Arg Ser Arg Leu Ser Ser
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Ala Ala Ala Lys Pro Ser Val Thr Ala
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<211> 1201

<212> DNA

<213> Arabidopsis thaliana

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 ctcttctcttt ttctctgtca ctaattttca g act gag aaa gct ttt ctt aag 167
 Thr Glu Lys Ala Phe Leu Lys
 5 10

cag cct aag gtc ttc ctt ag gtaattttgc gattcgattt ctctctgttc 217
 Gln Pro Lys Val Phe Leu Se
 15

tctattgttt cattgtattt aagttccaag ttgtttatat tgttcattgt ttctgattta 277

tcaag c tcg aag aaa tct gga aag gga aag aga cct gga aaa ggt gga 325
 r Ser Lys Lys Ser Gly Lys Gly Lys Arg Pro Gly Lys Gly Gly
 20 25 30

aac cgt ttc tgg aag aac att ggt ttg ggc ttc aag act cct cgt gaa 373
 Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg Glu
 35 40 45

gcc att gat g gtatgtttta gcttttaact cgttataata gataaggaac 423
 Ala Ile Asp G
 50

tcttggaattg tggtgttcat atagtcgata gatttcaaata gctattttgt cttgtagaat 483

cttaagcttt ggtttagtga gttctgattc ttcagcttta tctggatcta cattactgtt 543

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tcagtgatgc aaatgttatc agtagatttt gaattagtag gatgtcactg atttgaatat 603
gtgatcaagc ttcatagaaa cctgcatcat tctctatata cctttaagtc agattctcag 663
gttattgtgt atttgtgtgg aacag ga gct tac gtt gac aag aaa tgc ccc 714
                                ly Ala Tyr Val Asp Lys Lys Cys Pro
                                55                                60
ttc act gga act gtt tcc att aga ggt cgt atc tta gct ggt act tgc 762
Phe Thr Gly Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys
                                65                                70                                75
cac agt gcg aaa atg cag agg acc att atc gtg cga agg gat tac ctt 810
His Ser Ala Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu
                                80                                85                                90
cac ttt gtg aag aag tat cag ag gtaaattcat acattctcat acttctttcc 863
His Phe Val Lys Lys Tyr Gln Ar
                                95
atagagtctt acacattgat gtttaagaaa gtaatatcct ttttgttctt ag g tat 919
                                g Tyr
                                100
gag aag agg cat tca aac att ccg gct cat gtc tca cca tgc ttc cgt 967
Glu Lys Arg His Ser Asn Ile Pro Ala His Val Ser Pro Cys Phe Arg
                                105                                110                                115
gtt aag gaa gga gac cat atc atc att ggc caa tgc ag gttatgatct 1015
Val Lys Glu Gly Asp His Ile Ile Ile Gly Gln Cys Ar
                                120                                125
gattcaaacc tacaaattgt ctccattgat tctgattatc gtgaatttgt tttgatcttt 1075
ttgtttgtta atgattgata atttcag g cca ttg tgc aag aca gtg agg ttc 1127
                                g Pro Leu Ser Lys Thr Val Arg Phe
                                130                                135
aat gtg ttg aag gtg ata cca gct ggg tct tct tct tca ttt gga aag 1175
Asn Val Leu Lys Val Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys
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Lys Ala Phe Thr Gly Met
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<210> 30

<211> 160

<212> PRT

<213> Arabidopsis thaliana

<400> 30

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 Gly Asn Arg Phe Trp Lys Asn Ile Gly Leu Gly Phe Lys Thr Pro Arg
 35 40 45
 Glu Ala Ile Asp Gly Ala Tyr Val Asp Lys Lys Cys Pro Phe Thr Gly
 50 55 60
 Thr Val Ser Ile Arg Gly Arg Ile Leu Ala Gly Thr Cys His Ser Ala
 65 70 75 8
 Lys Met Gln Arg Thr Ile Ile Val Arg Arg Asp Tyr Leu His Phe Val
 85 90 95
 Lys Lys Tyr Gln Arg Tyr Glu Lys Arg His Ser Asn Ile Pro Ala His
 100 105 110
 Val Ser Pro Cys Phe Arg Val Lys Glu Gly Asp His Ile Ile Ile Gly
 115 120 125
 Gln Cys Arg Pro Leu Ser Lys Thr Val Arg Phe Asn Val Leu Lys Val
 130 135 140
 Ile Pro Ala Gly Ser Ser Ser Ser Phe Gly Lys Lys Ala Phe Thr Gly
 145 150 155 16
 Met

<210> 31
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 <212> DNA
 <213> Arabidopsis thaliana

<220>
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 <222> (23)..(1780)

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 Met Gly Ser Ile Glu Glu Glu Ala Arg Pro
 1 5 10

 ctc atc gaa gaa ggt tta att tta cag gaa gtg aaa ttg tat gct gaa 100
 Leu Ile Glu Glu Gly Leu Ile Leu Gln Glu Val Lys Leu Tyr Ala Glu
 15 20 25

 gat ggt tca gtg gac ttt aat gga aac cca cca ttg aag gag aaa aca 148
 Asp Gly Ser Val Asp Phe Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr
 30 35 40

 gga aac tgg aaa gct tgt cct ttt att ctt ggt aat gaa tgt tgt gag 196
 Gly Asn Trp Lys Ala Cys Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu
 45 50 55

agg cta gct tac tat ggt att gct ggg aat tta atc act tac ctc acc	244
Arg Leu Ala Tyr Tyr Gly Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr	
60 65 70	
act aag ctt cac caa gga aat gtt tct gct gct aca aac gtt acc aca	292
Thr Lys Leu His Gln Gly Asn Val Ser Ala Ala Thr Asn Val Thr Thr	
75 80 85 90	
tgg caa ggg act tgt tat ctc act cct ctc att gga gct gtt ctg gct	340
Trp Gln Gly Thr Cys Tyr Leu Thr Pro Leu Ile Gly Ala Val Leu Ala	
95 100 105	
gat gct tac tgg gga cgt tac tgg acc atc gct tgt ttc tcc ggg att	388
Asp Ala Tyr Trp Gly Arg Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile	
110 115 120	
tat ttc atc ggg atg tct gcg tta act ctt tca gct tca gtt ccg gca	436
Tyr Phe Ile Gly Met Ser Ala Leu Thr Leu Ser Ala Ser Val Pro Ala	
125 130 135	
ttg aag cca gcg gaa tgt att ggt gac ttt tgt cca tct gca acg cca	484
Leu Lys Pro Ala Glu Cys Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro	
140 145 150	
gct cag tat gcg atg ttc ttt ggt ggg ctt tac ctg atc gct ctt gga	532
Ala Gln Tyr Ala Met Phe Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly	
155 160 165 170	
act gga ggt atc aaa ccg tgt gtc tca tcc ttc ggt gcc gat cag ttt	580
Thr Gly Gly Ile Lys Pro Cys Val Ser Ser Phe Gly Ala Asp Gln Phe	
175 180 185	
gat gac acg gac tct cgg gaa cga gtt aga aaa gct tcg ttc ttt aac	628
Asp Asp Thr Asp Ser Arg Glu Arg Val Arg Lys Ala Ser Phe Phe Asn	
190 195 200	
tgg ttt tac ttc tcc atc aat att gga gca ctt gtg tca tct agt ctt	676
Trp Phe Tyr Phe Ser Ile Asn Ile Gly Ala Leu Val Ser Ser Ser Leu	
205 210 215	
cta gtt tgg att caa gag aat cgg ggg tgg ggt tta ggg ttt ggg ata	724
Leu Val Trp Ile Gln Glu Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile	
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cca aca gtg ttc atg gga cta gcc att gca agt ttc ttc ttt ggc aca	772
Pro Thr Val Phe Met Gly Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr	
235 240 245 250	
cct ctt tat agg ttt cag aaa cct gga gga agc cct ata act cgg att	820
Pro Leu Tyr Arg Phe Gln Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile	
255 260 265	
tcc caa gtc gtg gtt gct tcg ttc cgg aaa tcg tct gtc aaa gtc cct	868
Ser Gln Val Val Val Ala Ser Phe Arg Lys Ser Ser Val Lys Val Pro	
270 275 280	
gaa gac gcc aca ctt ctg tat gaa act caa gac aag aac tct gct att	916

Glu Asp Ala Thr Leu Leu Tyr	Glu Thr Gln Asp Lys Asn Ser Ala Ile	
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gct gga agt aga aaa atc gag cat acc gat gat tgc cag tat ctt gac		964
Ala Gly Ser Arg Lys Ile Glu His Thr Asp Asp Cys Gln Tyr Leu Asp		
300	305	310
aaa gcc gct gtt atc tca gaa gaa gaa tcg aaa tcc gga gat tat tcc		1012
Lys Ala Ala Val Ile Ser Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser		
315	320	325
aac tcg tgg aga cta tgc acg gtt acg caa gtc gaa gaa ctc aag att		1060
Asn Ser Trp Arg Leu Cys Thr Val Thr Gln Val Glu Glu Leu Lys Ile		
335	340	345
ctg atc cga atg ttc cca atc tgg gct tct ggt atc att ttc tca gct		1108
Leu Ile Arg Met Phe Pro Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala		
350	355	360
gta tac gca caa atg tcc aca atg ttt gtt caa caa gcc cga gcc atg		1156
Val Tyr Ala Gln Met Ser Thr Met Phe Val Gln Gln Gly Arg Ala Met		
365	370	375
aac tgc aaa att gga tca ttc cag ctt cct cct gca gca ctc ggg aca		1204
Asn Cys Lys Ile Gly Ser Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr		
380	385	390
ttc gac aca gca agc gtc atc atc tgg gtg ccg ctc tac gac cgg ttc		1252
Phe Asp Thr Ala Ser Val Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe		
395	400	410
atc gtt ccc tta gca aga aag ttc aca gga gta gac aaa gga ttc act		1300
Ile Val Pro Leu Ala Arg Lys Phe Thr Gly Val Asp Lys Gly Phe Thr		
415	420	425
gag ata caa aga atg gga att ggt ctg ttt gtc tct gtt ctc tgt atg		1348
Glu Ile Gln Arg Met Gly Ile Gly Leu Phe Val Ser Val Leu Cys Met		
430	435	440
gca gct gca gct atc gtc gaa atc atc cgt ctc cat atg gcc aac gat		1396
Ala Ala Ala Ala Ile Val Glu Ile Ile Arg Leu His Met Ala Asn Asp		
445	450	455
ctt gga tta gtc gag tca gga gcc cca gtt ccc ata tcc gtc ttg tgg		1444
Leu Gly Leu Val Glu Ser Gly Ala Pro Val Pro Ile Ser Val Leu Trp		
460	465	470
cag att cca cag tac ttc att ctc ggt gca gcc gaa gta ttc tac ttc		1492
Gln Ile Pro Gln Tyr Phe Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe		
475	480	485
atc ggt cag ctc gag ttc ttc tac gac caa tct cca gat gca atg aga		1540
Ile Gly Gln Leu Glu Phe Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg		
495	500	505
agc ttg tgc agt gcc tta gct ctt ttg acc aat gca ctt ggt aac tac		1588
Ser Leu Cys Ser Ala Leu Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr		

510	515	520	
ttg agc tcg ttg atc ctc acg ctc gtg act tat ttt aca aca aga aat			1636
Leu Ser Ser Leu Ile Leu Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn			
525	530	535	
ggg caa gaa ggt tgg att tcg gat aat ctc aat tca ggt cat ctc gat			1684
Gly Gln Glu Gly Trp Ile Ser Asp Asn Leu Asn Ser Gly His Leu Asp			
540	545	550	
tac ttc ttc tgg ctc ttg gct ggt ctt agc ctt gtg aac atg gcg gtt			1732
Tyr Phe Phe Trp Leu Leu Ala Gly Leu Ser Leu Val Asn Met Ala Val			
555	560	565	570
tac ttc ttc tct gct gct agg tat aag caa aag aaa gct tcg tcg tag			1780
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<213> Arabidopsis thaliana

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Asn Gly Asn Pro Pro Leu Lys Glu Lys Thr Gly Asn Trp Lys Ala Cys	
35 40 45	
Pro Phe Ile Leu Gly Asn Glu Cys Cys Glu Arg Leu Ala Tyr Tyr Gly	
50 55 60	
Ile Ala Gly Asn Leu Ile Thr Tyr Leu Thr Thr Lys Leu His Gln Gly	
65 70 75 80	
Asn Val Ser Ala Ala Thr Asn Val Thr Thr Trp Gln Gly Thr Cys Tyr	
85 90 95	
Leu Thr Pro Leu Ile Gly Ala Val Leu Ala Asp Ala Tyr Trp Gly Arg	
100 105 110	
Tyr Trp Thr Ile Ala Cys Phe Ser Gly Ile Tyr Phe Ile Gly Met Ser	
115 120 125	
Ala Leu Thr Leu Ser Ala Ser Val Pro Ala Leu Lys Pro Ala Glu Cys	
130 135 140	
Ile Gly Asp Phe Cys Pro Ser Ala Thr Pro Ala Gln Tyr Ala Met Phe	
145 150 155 160	

Phe Gly Gly Leu Tyr Leu Ile Ala Leu Gly Thr Gly Gly Ile Lys Pro
 165 170 175
 Cys Val Ser Ser Phe Gly Ala Asp Gln Phe Asp Asp Thr Asp Ser Arg
 180 185 190
 Glu Arg Val Arg Lys Ala Ser Phe Phe Asn Trp Phe Tyr Phe Ser Ile
 195 200 205
 Asn Ile Gly Ala Leu Val Ser Ser Ser Leu Leu Val Trp Ile Gln Glu
 210 215 220
 Asn Arg Gly Trp Gly Leu Gly Phe Gly Ile Pro Thr Val Phe Met Gly
 225 230 235 240
 Leu Ala Ile Ala Ser Phe Phe Phe Gly Thr Pro Leu Tyr Arg Phe Gln
 245 250 255
 Lys Pro Gly Gly Ser Pro Ile Thr Arg Ile Ser Gln Val Val Val Ala
 260 265 270
 Ser Phe Arg Lys Ser Ser Val Lys Val Pro Glu Asp Ala Thr Leu Leu
 275 280 285
 Tyr Glu Thr Gln Asp Lys Asn Ser Ala Ile Ala Gly Ser Arg Lys Ile
 290 295 300
 Glu His Thr Asp Asp Cys Gln Tyr Leu Asp Lys Ala Ala Val Ile Ser
 305 310 315 320
 Glu Glu Glu Ser Lys Ser Gly Asp Tyr Ser Asn Ser Trp Arg Leu Cys
 325 330 335
 Thr Val Thr Gln Val Glu Glu Leu Lys Ile Leu Ile Arg Met Phe Pro
 340 345 350
 Ile Trp Ala Ser Gly Ile Ile Phe Ser Ala Val Tyr Ala Gln Met Ser
 355 360 365
 Thr Met Phe Val Gln Gln Gly Arg Ala Met Asn Cys Lys Ile Gly Ser
 370 375 380
 Phe Gln Leu Pro Pro Ala Ala Leu Gly Thr Phe Asp Thr Ala Ser Val
 385 390 395 400
 Ile Ile Trp Val Pro Leu Tyr Asp Arg Phe Ile Val Pro Leu Ala Arg
 405 410 415
 Lys Phe Thr Gly Val Asp Lys Gly Phe Thr Glu Ile Gln Arg Met Gly
 420 425 430
 Ile Gly Leu Phe Val Ser Val Leu Cys Met Ala Ala Ala Ala Ile Val
 435 440 445
 Glu Ile Ile Arg Leu His Met Ala Asn Asp Leu Gly Leu Val Glu Ser
 450 455 460

Gly Ala Pro Val Pro Ile Ser Val Leu Trp Gln Ile Pro Gln Tyr Phe
 465 470 475 480
 Ile Leu Gly Ala Ala Glu Val Phe Tyr Phe Ile Gly Gln Leu Glu Phe
 485 490 495
 Phe Tyr Asp Gln Ser Pro Asp Ala Met Arg Ser Leu Cys Ser Ala Leu
 500 505 510
 Ala Leu Leu Thr Asn Ala Leu Gly Asn Tyr Leu Ser Ser Leu Ile Leu
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 Thr Leu Val Thr Tyr Phe Thr Thr Arg Asn Gly Gln Glu Gly Trp Ile
 530 535 540
 Ser Asp Asn Leu Asn Ser Gly His Leu Asp Tyr Phe Phe Trp Leu Leu
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 Leu Val Phe Arg Ser Ser Leu Ala Gly Asp Asp Gly Thr Ser Gly Gly
 15 20 25
 ggt ctt agc gga ttc gtc ggg aag att aac tct agt atc cgt agc tct 148
 Gly Leu Ser Gly Phe Val Gly Lys Ile Asn Ser Ser Ile Arg Ser Ser
 30 35 40
 cga att ggg ctc ttt tct aag ccg cct cca ggg ctt cct gct cct aga 196
 Arg Ile Gly Leu Phe Ser Lys Pro Pro Gly Leu Pro Ala Pro Arg
 45 50 55
 aaa gaa gaa gcg ccg tcg att cgg tgg agg aaa ggg gaa tta atc ggt 244
 Lys Glu Glu Ala Pro Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly
 60 65 70 75
 tgc ggt gct ttt gga aga gtt tac atg gga atg aac ctc gat tcc ggc 292

Cys	Gly	Ala	Phe	Gly	Arg	Val	Tyr	Met	Gly	Met	Asn	Leu	Asp	Ser	Gly		
				80					85					90			
gag	ctt	ctt	gca	att	aaa	cag	gtt	tta	atc	gct	cca	agc	agt	gct	tca	340	
Glu	Leu	Leu	Ala	Ile	Lys	Gln	Val	Leu	Ile	Ala	Pro	Ser	Ser	Ala	Ser		
			95					100					105				
aag	gag	aag	act	cag	ggt	cac	atc	cga	gag	ctt	gag	gaa	gaa	gta	caa	388	
Lys	Glu	Lys	Thr	Gln	Gly	His	Ile	Arg	Glu	Leu	Glu	Glu	Glu	Val	Gln		
		110					115					120					
ctt	ctt	aag	aat	ctt	tca	cat	ccg	aac	atc	gtt	aga	tac	ttg	ggt	act	436	
Leu	Leu	Lys	Asn	Leu	Ser	His	Pro	Asn	Ile	Val	Arg	Tyr	Leu	Gly	Thr		
	125					130					135						
gta	aga	gag	agt	gat	tcg	ttg	aat	att	ttg	atg	gag	ttt	gtt	cct	ggt	484	
Val	Arg	Glu	Ser	Asp	Ser	Leu	Asn	Ile	Leu	Met	Glu	Phe	Val	Pro	Gly		
140					145					150					155		
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Gly	Ser	Ile	Ser	Ser	Leu	Leu	Glu	Lys	Phe	Gly	Ser	Phe	Pro	Glu	Pro		
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gtg	att	att	atg	tac	aca	aag	caa	ctt	ctg	ctt	ggg	ctg	gaa	tat	ctt	580	
Val	Ile	Ile	Met	Tyr	Thr	Lys	Gln	Leu	Leu	Leu	Gly	Leu	Glu	Tyr	Leu		
			175					180					185				
cac	aac	aat	ggg	atc	atg	cat	cga	gat	att	aag	ggg	gca	aat	att	ttg	628	
His	Asn	Asn	Gly	Ile	Met	His	Arg	Asp	Ile	Lys	Gly	Ala	Asn	Ile	Leu		
		190					195					200					
gtc	gat	aac	aaa	ggt	tgc	atc	aga	ctc	gca	gat	ttt	ggg	gct	tcc	aag	676	
Val	Asp	Asn	Lys	Gly	Cys	Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ala	Ser	Lys		
	205					210					215						
aaa	gtt	gta	gag	cta	gct	act	gta	aat	ggt	gcc	aaa	tct	atg	aag	ggg	724	
Lys	Val	Val	Glu	Leu	Ala	Thr	Val	Asn	Gly	Ala	Lys	Ser	Met	Lys	Gly		
220					225					230					235		
acg	cct	tat	tgg	atg	gct	cct	gaa	gtc	att	ctc	cag	act	ggt	cat	agc	772	
Thr	Pro	Tyr	Trp	Met	Ala	Pro	Glu	Val	Ile	Leu	Gln	Thr	Gly	His	Ser		
				240					245					250			
ttc	tct	gct	gat	ata	tgg	agt	gtt	ggg	tgc	act	gtg	att	gag	atg	gct	820	
Phe	Ser	Ala	Asp	Ile	Trp	Ser	Val	Gly	Cys	Thr	Val	Ile	Glu	Met	Ala		
			255					260					265				
acg	ggg	aag	cct	ccc	tgg	agc	gag	cag	tat	cag	cag	ttt	gct	gct	gtc	868	
Thr	Gly	Lys	Pro	Pro	Trp	Ser	Glu	Gln	Tyr	Gln	Gln	Phe	Ala	Ala	Val		
		270					275					280					
ctt	cat	att	ggt	aga	aca	aaa	gct	cat	cct	cca	att	cca	gaa	gac	ctc	916	
Leu	His	Ile	Gly	Arg	Thr	Lys	Ala	His	Pro	Pro	Ile	Pro	Glu	Asp	Leu		
	285					290					295						
tca	cca	gag	gct	aaa	gac	ttt	cta	atg	aaa	tgc	tta	cac	aaa	gaa	cca	964	
Ser	Pro	Glu	Ala	Lys	Asp	Phe	Leu	Met	Lys	Cys	Leu	His	Lys	Glu	Pro		

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agc ttg aga ctc tct gca acc gaa ttg ctt cag cac ccg ttt gtc act				1012
Ser Leu Arg Leu Ser Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr	320	325	330	
gga aag cgc cag gaa cct tat cca gct tac cgt aat tct ctt acg gaa				1060
Gly Lys Arg Gln Glu Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu	335	340	345	
tgt gga aac cca ata act act caa gga atg aat gtt cgg agt tca ata				1108
Cys Gly Asn Pro Ile Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile	350	355	360	
aat tcg ttg atc agg agg tcg aca tgt tca ggc ttg aag gat gtc tgt				1156
Asn Ser Leu Ile Arg Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys	365	370	375	
gaa ctg gga agc ttg agg agt tcc att ata tac cca cag aag tca aat				1204
Glu Leu Gly Ser Leu Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn	380	385	390	395
aac tca gga ttt ggt tgg cga gat gga gac tct gat gac ctt tgt cag				1252
Asn Ser Gly Phe Gly Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln	400	405	410	
acc gat atg gat gat ctc tgc aac att gaa tca gtc aga aac aat gtt				1300
Thr Asp Met Asp Asp Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val	415	420	425	
ttg tca cag tcc acc gat tta aac aag agt ttt aat ccc atg tgt gat				1348
Leu Ser Gln Ser Thr Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp	430	435	440	
tcc acg gat aac tgg tct tgc aag ttt gat gaa agc cca aaa gtg atg				1396
Ser Thr Asp Asn Trp Ser Cys Lys Phe Asp Glu Ser Pro Lys Val Met	445	450	455	
aaa agc aaa tct aac ctg ctt tct tac caa gct tct caa ctc caa act				1444
Lys Ser Lys Ser Asn Leu Ser Tyr Gln Ala Ser Gln Leu Gln Thr	460	465	470	475
gga gtt cca tgt gat gag gaa acc agc tta aca ttt gct ggt ggc tct				1492
Gly Val Pro Cys Asp Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser	480	485	490	
tcc gtt gca gag gat gat tat aaa ggc aca gag ttg aaa ata aaa tca				1540
Ser Val Ala Glu Asp Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser	495	500	505	
ttt ttg gat gag aag gct cag gat ttg aaa agg ttg cag acc cct ctg				1588
Phe Leu Asp Glu Lys Ala Gln Asp Leu Lys Arg Leu Gln Thr Pro Leu	510	515	520	
ctt gaa gaa ttc cac aat gct atg aat cca gga ata ccc caa ggt gca				1636
Leu Glu Glu Phe His Asn Ala Met Asn Pro Gly Ile Pro Gln Gly Ala	525	530	535	

ctt gga gac acc aat atc tac aat tta cca aac tta cca agt ata agc 1684
 Leu Gly Asp Thr Asn Ile Tyr Asn Leu Pro Asn Leu Pro Ser Ile Ser
 540 545 550 555

 aag aca cct aaa cga ctt ccg agt aga cga ctc tca gca atc agt gat 1732
 Lys Thr Pro Lys Arg Leu Pro Ser Arg Arg Leu Ser Ala Ile Ser Asp
 560 565 570

 gct atg ccc agc cca ctc aaa agc tcc aaa cgt aca ctg aac aca agc 1780
 Ala Met Pro Ser Pro Leu Lys Ser Ser Lys Arg Thr Leu Asn Thr Ser
 575 580 585

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 590 595 600

 aag aag gga gta aat aat agc cgt tgt ttc tca gag ata cgt cgg aag 1876
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 605 610 615

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 620 625 630 635

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 35 40 45

 Ser Lys Pro Pro Pro Gly Leu Pro Ala Pro Arg Lys Glu Glu Ala Pro
 50 55 60

 Ser Ile Arg Trp Arg Lys Gly Glu Leu Ile Gly Cys Gly Ala Phe Gly
 65 70 75 80

 Arg Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Ile
 85 90 95

Lys Gln Val Leu Ile Ala Pro Ser Ser Ala Ser Lys Glu Lys Thr Gln
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 Gly His Ile Arg Glu Leu Glu Glu Glu Val Gln Leu Leu Lys Asn Leu
 115 120 125
 Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Ser Asp
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 Ser Leu Asn Ile Leu Met Glu Phe Val Pro Gly Gly Ser Ile Ser Ser
 145 150 155 160
 Leu Leu Glu Lys Phe Gly Ser Phe Pro Glu Pro Val Ile Ile Met Tyr
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 Thr Lys Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn Asn Gly Ile
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 Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly
 195 200 205
 Cys Ile Arg Leu Ala Asp Phe Gly Ala Ser Lys Lys Val Val Glu Leu
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 Ala Thr Val Asn Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met
 225 230 235 240
 Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile
 245 250 255
 Trp Ser Val Gly Cys Thr Val Ile Glu Met Ala Thr Gly Lys Pro Pro
 260 265 270
 Trp Ser Glu Gln Tyr Gln Gln Phe Ala Ala Val Leu His Ile Gly Arg
 275 280 285
 Thr Lys Ala His Pro Pro Ile Pro Glu Asp Leu Ser Pro Glu Ala Lys
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 Asp Phe Leu Met Lys Cys Leu His Lys Glu Pro Ser Leu Arg Leu Ser
 305 310 315 320
 Ala Thr Glu Leu Leu Gln His Pro Phe Val Thr Gly Lys Arg Gln Glu
 325 330 335
 Pro Tyr Pro Ala Tyr Arg Asn Ser Leu Thr Glu Cys Gly Asn Pro Ile
 340 345 350
 Thr Thr Gln Gly Met Asn Val Arg Ser Ser Ile Asn Ser Leu Ile Arg
 355 360 365
 Arg Ser Thr Cys Ser Gly Leu Lys Asp Val Cys Glu Leu Gly Ser Leu
 370 375 380
 Arg Ser Ser Ile Ile Tyr Pro Gln Lys Ser Asn Asn Ser Gly Phe Gly
 385 390 395 400

Trp Arg Asp Gly Asp Ser Asp Asp Leu Cys Gln Thr Asp Met Asp Asp
 405 410 415
 Leu Cys Asn Ile Glu Ser Val Arg Asn Asn Val Leu Ser Gln Ser Thr
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 Asp Leu Asn Lys Ser Phe Asn Pro Met Cys Asp Ser Thr Asp Asn Trp
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 Glu Glu Thr Ser Leu Thr Phe Ala Gly Gly Ser Ser Val Ala Glu Asp
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 Asp Tyr Lys Gly Thr Glu Leu Lys Ile Lys Ser Phe Leu Asp Glu Lys
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 545 550 555 560
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 565 570 575
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 580 585 590
 Gly Thr Glu Pro Thr Gln Val Asn Glu Ser Thr Lys Lys Gly Val Asn
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<222> (1)..(1605)

<400> 35

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agg gta gcg ggg gag gga gga ttg gat aca aca cca ccg ccg ccc cct	144
Arg Val Ala Gly Glu Gly Gly Leu Asp Thr Thr Pro Pro Pro Pro Pro	
35 40 45	
cca acg gca gat aca gtc gtg gcg gga agg acg agt tta ggt gag gcg	192
Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala	
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ccc cct cct cgt cag cct cca cgt cct cca aca gca ccg tgg tca gcg	240
Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala	
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Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg	
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cta gcg ctt gac gac caa cgt tgg ccg gat tgg aca acg aac ggt tgg	336
Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp	
100 105 110	
cta agc atg aga ccg acg tcc tcg cca aca agg cga att gac cca caa	384
Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln	
115 120 125	
ggg gcc cga cga tcc tca gtg tca cca gcg ccg gtg aca acg ggg atg	432
Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met	
130 135 140	
gcc acc tct cgc act gac gat acg cta ata gag gca gag acc ggt cgc	480
Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg	
145 150 155 160	
gac tgg acg agg aaa cga atg gtc agg aaa ttg ctt aaa gca agg gcg	528
Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala	
165 170 175	
aaa gac tac aag gag ggg gga att gcg gca tac ttt ggt tta cga gtg	576
Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val	
180 185 190	
ctg cga tgc tac tcg agg atc gta cga tcg atg aaa cgc cca ggc aac	624
Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn	
195 200 205	
ttg aaa ttc acg tgc cgg agg gat gtg gca ata gcc acg ttc agc ggc	672
Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly	

210	215	220	
aca ggc aga atg cag ctg agt atg aac agc cgt ttg cga gtc gag agc Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser 225 230 235 240			720
ctc gtg tcc gcg ggc cag agc gtg gcg tca ttc tgc ctt ttc ctg ata Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile 245 250 255			768
tgc acg gcg ccc tcg gcg atg cgg ctg gtt agc ctt ctt aca ctg acc Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr 260 265 270			816
cca agc atg acc tac cta aca tgc ggg ctg gga tgg atg acc gtc gtc Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val 275 280 285			864
gta ctg ccg gcg ata gtg gtc cac tgt tat atg cgc cga cat acg gaa Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu 290 295 300			912
ggg gga tgg cgg tat gcg gca ctc gag gag cat aag acg gag ccg gga Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly 305 310 315 320			960
cga aat gaa aag atc acc cgg agt aga cgc aac tcg gcg ttc ggc ggg Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly 325 330 335			1008
ctg gtc ggt cga aat aaa aga cga aag aag tcc aag gtc tcc ggg gca Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala 340 345 350			1056
ccg aca gcg gtt tac aca gcg atg ttt ttc atg ttc tcc acg gca atc Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile 355 360 365			1104
aag ggg atg gtg gtg tgc aca atg aaa aaa aaa gtc aaa aaa agt gcg Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala 370 375 380			1152
aat cgc aga ctc cgc cag ttg ctc cga tgg gcg cga tac cac gcg aac Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn 385 390 395 400			1200
gcg ttc ttg ctc tgt tct ctt gca tgc gca cga ttc gcg gca tcg cga Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg 405 410 415			1248
acg gtc atc cat tgc agt att tac cca cgt ttc ggc ccc tta gcc acg Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr 420 425 430			1296
gtg acg gcc ata tgt ttg ata cta cac acg tgt acg tac cga cgt acg Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr 435 440 445			1344

gag gca gac acg acg cga cac gaa aat gac gac gcc cgg aag gtg atg 1392
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
 450 455 460
 gaa gac atg gcc aaa cga atg gac gat agt agc agt ggg agc acg ttg 1440
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
 465 470 475 480
 agc acg ctc acg act gac gag acg tac cac acc acc acg gag gtg acc 1488
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
 485 490 495
 gat ttt gat tca tct cca tcg tgg gga cga tgc tca tcg cgg cgc ccg 1536
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
 500 505 510
 ccg gcg ctg ctg gaa tcg aca ttt cgg cga tcc ccg aga ggg tcg acg 1584
 Pro Ala Leu Leu Glu Ser Thr Phe Arg Arg Ser Pro Arg Gly Ser Thr
 515 520 525
 gga cga cga tgg cga gag tag attcggagtc aggaacgttg gaccgacagg 1635
 Gly Arg Arg Trp Arg Glu
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 35 40 45
 Pro Thr Ala Asp Thr Val Val Ala Gly Arg Thr Ser Leu Gly Glu Ala
 50 55 60
 Pro Pro Pro Arg Gln Pro Pro Arg Pro Pro Thr Ala Arg Trp Ser Ala
 65 70 75 80
 Met Gly Arg Val Met Cys Ser Pro Pro Ile Pro Leu Ser Arg Ser Arg
 85 90 95
 Leu Ala Leu Asp Asp Gln Arg Trp Pro Asp Trp Thr Thr Asn Gly Trp
 100 105 110

Leu Ser Met Arg Pro Thr Ser Ser Pro Thr Arg Arg Ile Asp Pro Gln
 115 120 125
 Gly Ala Arg Arg Ser Ser Val Ser Pro Ala Pro Val Thr Thr Gly Met
 130 135 140
 Ala Thr Ser Arg Thr Asp Asp Thr Leu Ile Glu Ala Glu Thr Gly Arg
 145 150 155 160
 Asp Trp Thr Arg Lys Arg Met Val Arg Lys Leu Leu Lys Ala Arg Ala
 165 170 175
 Lys Asp Tyr Lys Glu Gly Gly Ile Ala Ala Tyr Phe Gly Leu Arg Val
 180 185 190
 Leu Arg Cys Tyr Ser Arg Ile Val Arg Ser Met Lys Arg Pro Gly Asn
 195 200 205
 Leu Lys Phe Thr Cys Arg Arg Asp Val Ala Ile Ala Thr Phe Ser Gly
 210 215 220
 Thr Gly Arg Met Gln Leu Ser Met Asn Ser Arg Leu Arg Val Glu Ser
 225 230 235 240
 Leu Val Ser Ala Gly Gln Ser Val Ala Ser Phe Cys Leu Phe Leu Ile
 245 250 255
 Cys Thr Ala Pro Ser Ala Met Arg Leu Val Ser Leu Leu Thr Leu Thr
 260 265 270
 Pro Ser Met Thr Tyr Leu Thr Cys Gly Leu Gly Trp Met Thr Val Val
 275 280 285
 Val Leu Pro Ala Ile Val Val His Cys Tyr Met Arg Arg His Thr Glu
 290 295 300
 Gly Gly Trp Arg Tyr Ala Ala Leu Glu Glu His Lys Thr Glu Pro Gly
 305 310 315 320
 Arg Asn Glu Lys Ile Thr Arg Ser Arg Arg Asn Ser Ala Phe Gly Gly
 325 330 335
 Leu Val Gly Arg Asn Lys Arg Arg Lys Lys Ser Lys Val Ser Gly Ala
 340 345 350
 Pro Thr Ala Val Tyr Thr Ala Met Phe Phe Met Phe Ser Thr Ala Ile
 355 360 365
 Lys Gly Met Val Val Cys Thr Met Lys Lys Lys Val Lys Lys Ser Ala
 370 375 380
 Asn Arg Arg Leu Arg Gln Leu Leu Arg Trp Ala Arg Tyr His Ala Asn
 385 390 395 400
 Ala Phe Leu Leu Cys Ser Leu Ala Cys Ala Arg Phe Ala Ala Ser Arg
 405 410 415

Thr Val Ile His Cys Ser Ile Tyr Pro Arg Phe Gly Pro Leu Ala Thr
 420 425 430
 Val Thr Ala Ile Cys Leu Ile Leu His Thr Cys Thr Tyr Arg Arg Thr
 435 440 445
 Glu Ala Asp Thr Thr Arg His Glu Asn Asp Asp Ala Arg Lys Val Met
 450 455 460
 Glu Asp Met Ala Lys Arg Met Asp Asp Ser Ser Ser Gly Ser Thr Leu
 465 470 475 480
 Ser Thr Leu Thr Thr Asp Glu Thr Tyr His Thr Thr Thr Glu Val Thr
 485 490 495
 Asp Phe Asp Ser Ser Pro Ser Trp Gly Arg Cys Ser Ser Arg Arg Pro
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 Ala Lys Lys Gly Ala Asn Leu Phe Lys
 15 20
 ccgctgaaaa ttctcacggc gcattctatc ccgcagaact tttctgacca cttttag 155
 acc cgc tgc gct cag tgc cac acc ctg aag gcc ggc gag ggc aac aag 203
 Thr Arg Cys Ala Gln Cys His Thr Leu Lys Ala Gly Glu Gly Asn Lys
 25 30 35

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att ggc cct gag ctc cac ggt ctc ttc ggc cgc aag act ggt tcc gtc 251
Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys Thr Gly Ser Val
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gct ggc tac tca tac acc gac gcc aac aag cag aag ggt atc gag tgg 299
Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys Gly Ile Glu Trp
      55                      60                      65

aag gac gac act ctc gtacgtcacg ccaccggaag attgaaatgt ccccgagacc 354
Lys Asp Asp Thr Leu
      70

ctccgctaac acgacacag ttc gag tac ctc gag aac ccc aag aag tac att 406
      Phe Glu Tyr Leu Glu Asn Pro Lys Lys Tyr Ile
                      75                      80

ccc ggt acc aag atg gcc ttc ggt ggt ctc aag aag ccc aag gac cgc 454
Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys Pro Lys Asp Arg
      85                      90                      95                      100

aac gac ctc atc acc ttc ctt gag gag gag acc aaa taa gcgtcttgct 503
Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
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acccc 508

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Glu Gly Asn Lys Ile Gly Pro Glu Leu His Gly Leu Phe Gly Arg Lys
      35                      40                      45

Thr Gly Ser Val Ala Gly Tyr Ser Tyr Thr Asp Ala Asn Lys Gln Lys
      50                      55                      60

Gly Ile Glu Trp Lys Asp Asp Thr Leu Phe Glu Tyr Leu Glu Asn Pro
      65                      70                      75                      80

Lys Lys Tyr Ile Pro Gly Thr Lys Met Ala Phe Gly Gly Leu Lys Lys
      85                      90                      95

Pro Lys Asp Arg Asn Asp Leu Ile Thr Phe Leu Glu Glu Glu Thr Lys
      100                      105                      110

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 tta atc aga act cca caa aca aaa caa cgt ctc aat ttc cac tca aaa 96
 Leu Ile Arg Thr Pro Gln Thr Lys Gln Arg Leu Asn Phe His Ser Lys
 20 25 30
 acc cca aac cca gac gga tct aaa gat cca tct cca ccg gag cat cca 144
 Thr Pro Asn Pro Asp Gly Ser Lys Asp Pro Ser Pro Pro Glu His Pro
 35 40 45

77

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gtt gaa gta atc ggc cgg atc cga gat tac cct gac cgg aaa gag aaa 192
Val Glu Val Ile Gly Arg Ile Arg Asp Tyr Pro Asp Arg Lys Glu Lys
    50                55                60

tca cct tcg atc tta caa gtc aac aca gat aat caa acg gta cga gtc 240
Ser Pro Ser Ile Leu Gln Val Asn Thr Asp Asn Gln Thr Val Arg Val
    65                70                75                80

aga gct gat gtt ggg tac aga gac ttc aca ctc gac ggt gtt tct ttc 288
Arg Ala Asp Val Gly Tyr Arg Asp Phe Thr Leu Asp Gly Val Ser Phe
                85                90                95

tcg gag caa gaa ggt ctt gaa gag ttc tac aag aag ttt ata gaa gag 336
Ser Glu Gln Gly Leu Glu Glu Phe Tyr Lys Lys Phe Ile Glu Glu
    100                105                110

agg att aaa gga gtg aaa gtt ggg aat aaa tgc acg att atg atg tat 384
Arg Ile Lys Gly Val Lys Val Gly Asn Lys Cys Thr Ile Met Met Tyr
    115                120                125

gga cct act ggt gct gga aag agt cat act atg ttt ggt tgt ggg aaa 432
Gly Pro Thr Gly Ala Gly Lys Ser His Thr Met Phe Gly Cys Gly Lys
    130                135                140

gag cct ggg att gtg tat cgt tct ttg aga gat ata ttg gga gat tct 480
Glu Pro Gly Ile Val Tyr Arg Ser Leu Arg Asp Ile Leu Gly Asp Ser
    145                150                155                160

gat caa gat ggt gtt act ttt gtt caa gtt act gtt ctt gag gtt tat 528
Asp Gln Asp Gly Val Thr Phe Val Gln Val Thr Val Leu Glu Val Tyr
                165                170                175

aat gag gag att tat gat ctt ctt tcg act aat agt agt aac aat tta 576
Asn Glu Glu Ile Tyr Asp Leu Leu Ser Thr Asn Ser Ser Asn Asn Leu
                180                185                190

ggt att ggt tgg cct aaa gga gca agc act aag gtaaagtttc ttgattgata 629
Gly Ile Gly Trp Pro Lys Gly Ala Ser Thr Lys
    195                200

acttttagtat acattgaatt ggctttaaag gtgtgtactt tggtgttttg ttacag gtg 688
Val

agg ctt gaa gta atg ggg aaa aag gcg aaa aac gca agt ttt att tct 736
Arg Leu Glu Val Met Gly Lys Lys Ala Lys Asn Ala Ser Phe Ile Ser
    205                210                215                220

ggg aca gag gct ggg aag att tct aaa gaa att gtc aaa gtg gag aaa 784
Gly Thr Glu Ala Gly Lys Ile Ser Lys Glu Ile Val Lys Val Glu Lys
                225                230                235

cgg aga att gtg aag agt aca ctt tgt aac gaa aga agt tct cgg agt 832
Arg Arg Ile Val Lys Ser Thr Leu Cys Asn Glu Arg Ser Ser Arg Ser
                240                245                250

cac tgc att gtaagaacga tcttcttgat tgatgtgtat gcatagcttt 881

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His Cys Ile
255

atgcagctta tctctgtttt aacttactag tgtgggtggt tctttttgta g atc ata 938
Ile Ile

ctt gat gtg cca act gtt ggg gga aga ttg atg ctt gtt gac atg gct 986
Leu Asp Val Pro Thr Val Gly Gly Arg Leu Met Leu Val Asp Met Ala
260 265 270

ggt tct gaa aat ata gac caa gct ggg cag act gga ttt gaa gct aag 1034
Gly Ser Glu Asn Ile Asp Gln Ala Gly Gln Thr Gly Phe Glu Ala Lys
275 280 285

atg caa gtaatgtttc ctctctcaat ttgtttgatt ctactaaagt tattgtagtt 1090
Met Gln
290

atggatatca actgacttat atctctcatt attcaacag act gct aag atc aac 1144
Thr Ala Lys Ile Asn
295

cag gga aat att gca ctg aag cga gtt gtg gaa tct ata gca aat gga 1192
Gln Gly Asn Ile Ala Leu Lys Arg Val Val Glu Ser Ile Ala Asn Gly
300 305 310

gat tct cat gta ccc ttt aga gac agc aag ctg acc atg ctt ctc cag 1240
Asp Ser His Val Pro Phe Arg Asp Ser Lys Leu Thr Met Leu Leu Gln
315 320 325

gtgaaattct tgttccattg ttttatcttc tggaaaatgt tttacgtggt gcttggtttt 1300

cttgaagata tttagtgttg tttctattct ctgaatgcag gac tct ttt gaa gat 1355
Asp Ser Phe Glu Asp
330

gac aag tca aag att cta atg atc ctg tgt gcg agc ccg gat cca aag 1403
Asp Lys Ser Lys Ile Leu Met Ile Leu Cys Ala Ser Pro Asp Pro Lys
335 340 345

gaa atg cac aag act ctc tgt act cta gag tat ggg gca aaa gca aag 1451
Glu Met His Lys Thr Leu Cys Thr Leu Glu Tyr Gly Ala Lys Ala Lys
350 355 360 365

tgc ata gtt cgt ggg tct cat act cca aac aaa gat aag tat ggg ggt 1499
Cys Ile Val Arg Gly Ser His Thr Pro Asn Lys Asp Lys Tyr Gly Gly
370 375 380

gat gag tct gct tct gct gtg att ttg gga tca aga ata gct gcc atg 1547
Asp Glu Ser Ala Ser Ala Val Ile Leu Gly Ser Arg Ile Ala Ala Met
385 390 395

gat gag ttc att atc aaa ctc cag tct gag aag aag caa aaa gaa aaa 1595
Asp Glu Phe Ile Ile Lys Leu Gln Ser Glu Lys Lys Gln Lys Glu Lys
400 405 410

gaa agg aat gag gca caa aag cag ctg aag aag aag gaa gag gaa gtt 1643

79

Glu Arg Asn Glu Ala Gln Lys Gln Leu Lys Lys Lys Glu Glu Glu Val	
415 420 425	
gct gct tta aga tct ctt tta aca cag agg gaa gct tgt gct acc aat	1691
Ala Ala Leu Arg Ser Leu Leu Thr Gln Arg Glu Ala Cys Ala Thr Asn	
430 435 440 445	
gaa gag gag ata aaa gag aaa gta aac gag aga acc cag ctt ttg aag	1739
Glu Glu Glu Ile Lys Glu Lys Val Asn Glu Arg Thr Gln Leu Leu Lys	
450 455 460	
tcg gaa cta gat aag aaa ctt gaa gaa tgc cga aga atg gct gag gaa	1787
Ser Glu Leu Asp Lys Lys Leu Glu Glu Cys Arg Arg Met Ala Glu Glu	
465 470 475	
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Phe Val Glu Met Glu Arg Arg Arg Met Glu Glu Arg Ile Val Gln Gln	
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Gln Glu Glu Leu Glu Met Met Arg Arg Arg Leu Glu Glu Ile Glu Val	
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Glu Phe Arg Arg Ser Asn Gly Gly Ser Val Asp Glu Thr Ser Gly Phe	
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Ala Lys Arg Leu Arg Ser Leu Tyr Ser Asp Asp Asp Pro Gly Met Val	
530 535 540	
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Lys Ser Met Asp Leu Asp Met Gly Asp Pro Glu Pro Val Lys Gln Val	
545 550 555	
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Trp Gly Ala Val Ser His Gln Ser Ser Asn Thr Ile Ser Ser Asn Phe	
560 565 570	
act aac ctt ttg caa ccg aag cct tca gag aat atg ctt aca cag atg	2123
Thr Asn Leu Leu Gln Pro Lys Pro Ser Glu Asn Met Leu Thr Gln Met	
575 580 585	
tat cct gac cgg gta tgc ttg agc act gtc ttt gaa gaa gaa gaa gtt	2171
Tyr Pro Asp Arg Val Cys Leu Ser Thr Val Phe Glu Glu Glu Glu Val	
590 595 600 605	
gaa gaa gag gaa gaa aaa gtg ata gtc gag gat aaa agc atc tgc ttg	2219
Glu Glu Glu Glu Glu Lys Val Ile Val Glu Asp Lys Ser Ile Cys Leu	
610 615 620	
ata aca aca cca atg cct agt ttg aac tct gaa ggt ttg ggt aaa gag	2267
Ile Thr Thr Pro Met Pro Ser Leu Asn Ser Glu Gly Leu Gly Lys Glu	
625 630 635	
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82

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 930 935
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Val	Glu	Gly	Gly	Trp	Leu	Leu	Arg	Tyr	Met	His	Ala	Asn	Gly	Ala	Ser		
		80					85					90					
atg	ttt	ctt	att	gtg	gtt	tac	ctt	cat	att	ttt	cgt	ggg	cta	tat	cat	338	
Met	Phe	Leu	Ile	Val	Val	Tyr	Leu	His	Ile	Phe	Arg	Gly	Leu	Tyr	His		
	95					100					105						
gcg	agt	tat	agc	agt	cct	agg	gaa	ttt	gtt	tgg	tgt	ctt	gga	gtt	gta	386	
Ala	Ser	Tyr	Ser	Ser	Pro	Arg	Glu	Phe	Val	Trp	Cys	Leu	Gly	Val	Val		
110					115					120					125		
atc	ttc	cta	tta	atg	att	gtg	aca	gct	ttt	ata	gga	tat	gta	cta	cct	434	
Ile	Phe	Leu	Leu	Met	Ile	Val	Thr	Ala	Phe	Ile	Gly	Tyr	Val	Leu	Pro		
				130					135						140		
tgg	ggg	cag	atg	agc	ttt	tgg	gga	gct	aca	gta	att	aca	agc	tta	gct	482	
Trp	Gly	Gln	Met	Ser	Phe	Trp	Gly	Ala	Thr	Val	Ile	Thr	Ser	Leu	Ala		
			145					150					155				
agc	gcc	ata	cct	gta	gta	gga	gat	acc	ata	gtg	act	tgg	ctt	tgg	ggg	530	
Ser	Ala	Ile	Pro	Val	Val	Gly	Asp	Thr	Ile	Val	Thr	Trp	Leu	Trp	Gly		
		160					165					170					
ggg	ttc	tcc	gtg	gac	aat	gcc	acc	tta	aat	cgt	ttt	ttt	agt	ctt	cat	578	
Gly	Phe	Ser	Val	Asp	Asn	Ala	Thr	Leu	Asn	Arg	Phe	Phe	Ser	Leu	His		
	175					180					185						
cat	tta	ctc	ccc	ttt	att	tta	gta	ggc	gcc	agt	ctt	ctt	cat	ctg	gcc	626	
His	Leu	Leu	Pro	Phe	Ile	Leu	Val	Gly	Ala	Ser	Leu	Leu	His	Leu	Ala		
190					195					200					205		
gca	ttg	cat	caa	tat	gga	tca	aat	aat	cca	ttg	ggg	gta	cat	tct	gag	674	
Ala	Leu	His	Gln	Tyr	Gly	Ser	Asn	Asn	Pro	Leu	Gly	Val	His	Ser	Glu		
			210						215					220			
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Met	Asp	Lys	Ile	Ala	Phe	Tyr	Pro	Tyr	Phe	Tyr	Val	Lys	Asp	Leu	Val		
			225					230					235				
ggg	tgg	gta	gct	ttt	gct	atc	ttt	ttt	tct	att	tgg	att	ttt	tat	gct	770	
Gly	Trp	Val	Ala	Phe	Ala	Ile	Phe	Phe	Ser	Ile	Trp	Ile	Phe	Tyr	Ala		
		240				245						250					
cct	aat	gtt	ttg	gga	cat	ccc	gac	aat	tat	ata	cct	gct	aat	ccg	atg	818	
Pro	Asn	Val	Leu	Gly	His	Pro	Asp	Asn	Tyr	Ile	Pro	Ala	Asn	Pro	Met		
		255				260					265						
tcc	acc	ccg	cct	cat	att	gtg	ccg	gaa	tgg	tat	ttc	cta	ccg	atc	cat	866	
Ser	Thr	Pro	Pro	His	Ile	Val	Pro	Glu	Trp	Tyr	Phe	Leu	Pro	Ile	His		
270					275					280					285		
gcc	att	ctt	cgt	agt	ata	cct	gac	aaa	gcg	gga	ggg	gta	gcc	gca	ata	914	
Ala	Ile	Leu	Arg	Ser	Ile	Pro	Asp	Lys	Ala	Gly	Gly	Val	Ala	Ala	Ile		

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gca cca gtt ttt ata tgt ctc ttg gct tta cct ttt ttt aaa agt atg			962
Ala Pro Val Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met			
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tat gtg cgt agt tca agt ttt cga ccg att cac caa gga atg ttt tgg			1010
Tyr Val Arg Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp			
320	325	330	
ttg ctt ttg gcg gat tgc tta cta cta ggt tgg atc gga tgt caa cct			1058
Leu Leu Leu Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro			
335	340	345	
gtg gag gct cca ttt gtt act att gga caa att tct cct ttg gtt ttc			1106
Val Glu Ala Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe			
350	355	360	365
ttc ttg ttc ttt gcc ata acg ccc att ctg gga cga gtt gga aga gga			1154
Phe Leu Phe Phe Ala Ile Thr Pro Ile Leu Gly Arg Val Gly Arg Gly			
370	375	380	
att cct aat tct tac acg gat gag act gat cac acc tga tcagtgaata			1203
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Ser Tyr Trp Trp Gly Phe Gly Pro Leu Ala Gly Ile Cys Leu Val Ile	
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Gln Ile Val Thr Gly Val Phe Leu Ala Met His Tyr Thr Pro His Val	
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Asp Leu Ala Phe Asn Ser Val Glu His Ile Met Arg Asp Val Glu Gly	
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Gly Trp Leu Leu Arg Tyr Met His Ala Asn Gly Ala Ser Met Phe Leu	
85 90 95	
Ile Val Val Tyr Leu His Ile Phe Arg Gly Leu Tyr His Ala Ser Tyr	
100 105 110	
Ser Ser Pro Arg Glu Phe Val Trp Cys Leu Gly Val Val Ile Phe Leu	
115 120 125	

Leu Met Ile Val Thr Ala Phe Ile Gly Tyr Val Leu Pro Trp Gly Gln
 130 135 140
 Met Ser Phe Trp Gly Ala Thr Val Ile Thr Ser Leu Ala Ser Ala Ile
 145 150 155 160
 Pro Val Val Gly Asp Thr Ile Val Thr Trp Leu Trp Gly Gly Phe Ser
 165 170 175
 Val Asp Asn Ala Thr Leu Asn Arg Phe Phe Ser Leu His His Leu Leu
 180 185 190
 Pro Phe Ile Leu Val Gly Ala Ser Leu Leu His Leu Ala Ala Leu His
 195 200 205
 Gln Tyr Gly Ser Asn Asn Pro Leu Gly Val His Ser Glu Met Asp Lys
 210 215 220
 Ile Ala Phe Tyr Pro Tyr Phe Tyr Val Lys Asp Leu Val Gly Trp Val
 225 230 235 240
 Ala Phe Ala Ile Phe Phe Ser Ile Trp Ile Phe Tyr Ala Pro Asn Val
 245 250 255
 Leu Gly His Pro Asp Asn Tyr Ile Pro Ala Asn Pro Met Ser Thr Pro
 260 265 270
 Pro His Ile Val Pro Glu Trp Tyr Phe Leu Pro Ile His Ala Ile Leu
 275 280 285
 Arg Ser Ile Pro Asp Lys Ala Gly Gly Val Ala Ala Ile Ala Pro Val
 290 295 300
 Phe Ile Cys Leu Leu Ala Leu Pro Phe Phe Lys Ser Met Tyr Val Arg
 305 310 315 320
 Ser Ser Ser Phe Arg Pro Ile His Gln Gly Met Phe Trp Leu Leu Leu
 325 330 335
 Ala Asp Cys Leu Leu Leu Gly Trp Ile Gly Cys Gln Pro Val Glu Ala
 340 345 350
 Pro Phe Val Thr Ile Gly Gln Ile Ser Pro Leu Val Phe Phe Leu Phe
 355 360 365
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cga gga aat tac gca gct aca ctc gat gtg tcg tat ccg gta ttc ccg      96
Arg Gly Asn Tyr Ala Ala Thr Leu Asp Val Ser Tyr Pro Val Phe Pro
               20               25               30

caa aat aaa gat ggc cgt gca ctt cag aaa gtt ctc gga acc att cgt     144
Gln Asn Lys Asp Gly Arg Ala Leu Gln Lys Val Leu Gly Thr Ile Arg
               35               40               45

aac gga gat ttg gct gtt tcg gct cct aaa aca agt ctt agg gca ggt     192
Asn Gly Asp Leu Ala Val Ser Ala Pro Lys Thr Ser Leu Arg Ala Gly
   50               55               60

att ttc ggt gaa ggt tcc agc ttg gtc gat cag atg ccc tgt aaa gtt     240
Ile Phe Gly Glu Gly Ser Ser Leu Val Asp Gln Met Pro Cys Lys Val
   65               70               75               80

tac gtg gcg ttc cac aaa gaa tca tac tgc tcg ctt acc ggg cta agc     288
Tyr Val Ala Phe His Lys Glu Ser Tyr Cys Ser Leu Thr Gly Leu Ser
               85               90               95

aaa cgc gga gtc gca ata aac gaa gca agt ctt tcc ctg gtc gga atc     336
Lys Arg Gly Val Ala Ile Asn Glu Ala Ser Leu Ser Leu Val Gly Ile
               100              105              110

act aaa gtt aga gcc ccc gtc gga aat acc gtt gga gcg gaa gca acc     384
Thr Lys Val Arg Ala Pro Val Gly Asn Thr Val Gly Ala Glu Ala Thr
               115              120              125

gta tac ata ggt agt cca aaa cct tat aca gag tgt agt act cca aat     432
Val Tyr Ile Gly Ser Pro Lys Pro Tyr Thr Glu Cys Ser Thr Pro Asn
               130              135              140

aaa atg tat gcg gtt gca gct ggt ttc aag gtg gca agt ttc gcc gct     480
Lys Met Tyr Ala Val Ala Ala Gly Phe Lys Val Ala Ser Phe Ala Ala
               145              150              155              160

agt acg tgc gta cgt ccg cct gca cgt gca cgt cgt acg ctg acc gtg     528
Ser Thr Cys Val Arg Pro Pro Ala Arg Ala Arg Arg Thr Leu Thr Val
               165              170              175

acg tcg acc gtg acg ctg tct atg gca act ggt aaa tgc gta aat aca     576
Thr Ser Thr Val Thr Leu Ser Met Ala Thr Gly Lys Cys Val Asn Thr
               180              185              190

gga aac gaa cca gta tct aaa cct aca gga gta cgt atg atg tta att     624
Gly Asn Glu Pro Val Ser Lys Pro Thr Gly Val Arg Met Met Leu Ile
               195              200              205

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gcg ata gtt tcc cgg cct gca aaa att ttc aat agc gta gga aat tta 720
Ala Ile Val Ser Arg Pro Ala Lys Ile Phe Asn Ser Val Gly Asn Leu
225 230 235 240

gaa cgt cct tca att tcg cat tct tgt gga caa ggt ttg gat gaa gct 768
Glu Arg Pro Ser Ile Ser His Ser Cys Gly Gln Gly Leu Asp Glu Ala
245 250 255

gcc gct tat atc aag ggt aga ctt tct cca atc gtt aaa gca gaa aga 816
Ala Ala Tyr Ile Lys Gly Arg Leu Ser Pro Ile Val Lys Ala Glu Arg
260 265 270

att aaa gtt ttg gtt aaa gac gag cac gaa gaa gta aaa gaa ctt ctt 864
Ile Lys Val Leu Val Lys Asp Glu His Glu Glu Val Lys Glu Leu Leu
275 280 285

caa gaa ggt tac gaa gaa atc gtc ggt gag tct cca agt ttc aat tta 912
Gln Glu Gly Tyr Glu Glu Ile Val Gly Glu Ser Pro Ser Phe Asn Leu
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gca caa gaa gcg tgg gaa aaa gct gaa aga cga gca aaa ggt cag tcc 960
Ala Gln Glu Ala Trp Glu Lys Ala Glu Arg Arg Ala Lys Gly Gln Ser
305 310 315 320

ccg tgc agt gcg gca aaa gca aac ctt gca acc tac tat ttt tca aca 1008
Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
325 330 335

ggg gat ttc gaa aaa tca att aaa ctc tac gaa gaa cct atg ggt ttg 1056
Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
340 345 350

aaa gat act gat aag agc tat ctg cga gaa cgt aga aaa aga gta gag 1104
Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
355 360 365

gct act acg ttg cgt gca ccg ttc gtg gtc cag ctg acc gtg cgt agt 1152
Ala Thr Thr Leu Arg Ala Pro Phe Val Val Gln Leu Thr Val Arg Ser
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Gln Asn Lys Asp	Gly Arg Ala Leu Gln	Lys Val Leu Gly	Thr Ile Arg
	35	40	45
Asn Gly Asp Leu	Ala Val Ser Ala	Pro Lys Thr Ser	Leu Arg Ala Gly
	50	55	60
Ile Phe Gly Glu	Gly Ser Ser Leu	Val Asp Gln Met	Pro Cys Lys Val
	65	70	75
Tyr Val Ala Phe	His Lys Glu Ser	Tyr Cys Ser Leu	Thr Gly Leu Ser
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Lys Arg Gly Val	Ala Ile Asn Glu	Ala Ser Leu Ser	Leu Val Gly Ile
	100	105	110
Thr Lys Val Arg	Ala Pro Val Gly	Asn Thr Val Gly	Ala Glu Ala Thr
	115	120	125
Val Tyr Ile Gly	Ser Pro Lys Pro	Tyr Thr Glu Cys	Ser Thr Pro Asn
	130	135	140
Lys Met Tyr Ala	Val Ala Ala Gly	Phe Lys Val Ala	Ser Phe Ala Ala
	145	150	155
Ser Thr Cys Val	Arg Pro Pro Ala	Arg Ala Arg Arg	Thr Leu Thr Val
	165	170	175
Thr Ser Thr Val	Thr Leu Ser Met	Ala Thr Gly Lys	Cys Val Asn Thr
	180	185	190
Gly Asn Glu Pro	Val Ser Lys Pro	Thr Gly Val Arg	Met Met Leu Ile
	195	200	205
Pro Leu Asp Ala	Thr Leu Ile Lys	Val Trp Thr Gly	Glu Val Lys Lys
	210	215	220
Ala Ile Val Ser	Arg Pro Ala Lys	Ile Phe Asn Ser	Val Gly Asn Leu
	225	230	235
Glu Arg Pro Ser	Ile Ser His Ser	Cys Gly Gln Gly	Leu Asp Glu Ala
	245	250	255
Ala Ala Tyr Ile	Lys Gly Arg Leu	Ser Pro Ile Val	Lys Ala Glu Arg
	260	265	270
Ile Lys Val Leu	Val Lys Asp Glu	His Glu Glu Val	Lys Glu Leu Leu
	275	280	285
Gln Glu Gly Tyr	Glu Glu Ile Val	Gly Glu Ser Pro	Ser Phe Asn Leu
	290	295	300
Ala Gln Glu Ala	Trp Glu Lys Ala	Glu Arg Arg Ala	Lys Gly Gln Ser

305 310 315 320
 Pro Cys Ser Ala Ala Lys Ala Asn Leu Ala Thr Tyr Tyr Phe Ser Thr
 325 330 335
 Gly Asp Phe Glu Lys Ser Ile Lys Leu Tyr Glu Glu Pro Met Gly Leu
 340 345 350
 Lys Asp Thr Asp Lys Ser Tyr Leu Arg Glu Arg Arg Lys Arg Val Glu
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 Val Val Phe Ser Val Ala Leu Leu Leu Phe Tyr Phe Ser Glu Thr Ser
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 cta gga gct cct tgt ccc atc aat ggc ttg cca atc gtg agg aat att 145
 Leu Gly Ala Pro Cys Pro Ile Asn Gly Leu Pro Ile Val Arg Asn Ile
 35 40 45
 agt gac ctt cct cag gat aac tat gga aga cca ggt ctt tcc cac atg 193
 Ser Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met
 50 55 60
 act gtt gct ggc tcc gta ttg cat gga atg aaa gag gtt gaa ata tgg 241
 Thr Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp
 65 70 75
 ctt cag aca ttt gct cca ggt tca gag aca cca att cac agg cac tcc 289
 Leu Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser
 80 85 90 95
 tgt gaa gag gtt ttt gtt gtc cta aag ggc agt ggt act ctg tat ctc 337
 Cys Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu
 100 105 110

gct gaa aca cat gga aat ttc cct ggg aaa cca atc gaa ttt cca atc 385
 Ala Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile
 115 120 125

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 Phe Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val
 130 135 140

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 Lys Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg
 145 150 155

ccg cct att aaa atc ttc atc tac gaa gac tgg ttt atg cca cac act 529
 Pro Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr
 160 165 170 175

gct gca agg ctg aag ttc cct tac tat tgg gat gag caa tgc att caa 577
 Ala Ala Arg Leu Lys Phe Pro Tyr Tyr Trp Asp Glu Gln Cys Ile Gln
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 35 40 45

Asp Leu Pro Gln Asp Asn Tyr Gly Arg Pro Gly Leu Ser His Met Thr
 50 55 60

Val Ala Gly Ser Val Leu His Gly Met Lys Glu Val Glu Ile Trp Leu
 65 70 75 80

Gln Thr Phe Ala Pro Gly Ser Glu Thr Pro Ile His Arg His Ser Cys
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Glu Glu Val Phe Val Val Leu Lys Gly Ser Gly Thr Leu Tyr Leu Ala
 100 105 110

Glu Thr His Gly Asn Phe Pro Gly Lys Pro Ile Glu Phe Pro Ile Phe
 115 120 125

Ala Asn Ser Thr Ile His Ile Pro Ile Asn Asp Ala His Gln Val Lys
 130 135 140

Asn Thr Gly His Glu Asp Leu Gln Val Leu Val Ile Ile Ser Arg Pro
 145 150 155 160
 Pro Ile Lys Ile Phe Ile Tyr Glu Asp Trp Phe Met Pro His Thr Ala
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 Pro Cys Arg Gly Ala Ser Ile Thr Gly Ser Leu Arg Asp Arg Arg Pro
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 Thr Ala Ile Leu Ile Gly Thr Leu Thr Ala Leu Gly Gly Gly Val Arg
 35 40 45
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 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
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 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
 65 70 75 80
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 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
 85 90 95
 ggt gga ccc gac ttc gat tgt gat gat ggt ggt gac gat ccg ctt ttg 336
 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu
 100 105 110
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 Ile Gln Asp Gly Val Lys Ala Ala Glu Glu Tyr Ala Lys Ser Gly Lys
 115 120 125

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Val Pro Asp Pro Ser Cys Thr Asp Asn Ala Glu Phe Gln Val Val Leu	
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att att att agg gag ggg ttg aaa act gat cct tta aaa tac act aag	480
Ile Ile Ile Arg Glu Gly Leu Lys Thr Asp Pro Leu Lys Tyr Thr Lys	
145 150 155 160	
cga ccc agt tgc ctt gtt ggt gtt tct gag gaa act act act ggt gtt	528
Arg Pro Ser Cys Leu Val Gly Val Ser Glu Glu Thr Thr Thr Gly Val	
165 170 175	
aag aga agt tac caa atg cag ccg aaa tgt act ttg ctt ttg cat gct	576
Lys Arg Ser Tyr Gln Met Gln Pro Lys Cys Thr Leu Leu Leu His Ala	
180 185 190	
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Thr Asp Val Cys Asp Thr Val Ile Lys Ser Lys Ile Asp Asn Leu Tyr	
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Arg Arg Pro Cys Lys Val Ala Leu Val Gly Gly Tyr Gly Asp Val Phe	
225 230 235 240	
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Lys Gly Trp Val Ala Ala Leu Lys Gln Ala Gly Ala Arg Val Ile Val	
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Thr Glu Ile Pro Gln Ile Cys Ala Val Gln Ala Thr Met Glu Gly Ser	
260 265 270	
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Ser Val Leu Thr Leu Glu Asp Val Val Ser Asp Val Asp Arg Phe Val	
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Thr Thr Thr Gly Asn Lys Asp Leu Ile Met Val Asp His Met Arg Arg	
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Met Lys Asn Gln Ala Ile Val Cys Asn Ile Arg Arg Phe Asp Asn Glu	
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Ile Asp Met Arg Ser Leu Glu Thr Phe Pro Gly Val Lys Arg Ile Thr	
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Ile Lys Ala Gln Thr Asp Arg Trp Val Phe Arg Asp Thr Asn Arg Gly	
340 345 350	
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 Ser Gln Leu Glu Leu Trp Arg Glu Lys Ser Thr Gly Lys Tyr Glu Lys
 385 390 395 400
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 Lys Val Tyr Val Phe Pro Lys His Leu Glu Lys Lys Val Ala Ala Leu
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 His Leu Val Lys Leu Gly Ala Arg Leu Thr Lys Leu Ser Arg Cys Thr
 420 425 430
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 Leu Leu Cys Thr Asp Asp Pro Val Glu Gly Arg Lys Glu Pro Pro His
 435 440 445
 cgt gct ggc agc cct gaa ccg tgc cag ctg cag ctg acc gtg ttc agg 1392
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 35 40 45
 Cys Gly Ser Cys Pro Ser Val Asp Arg Cys Gly His Ala Ser Ala Ala
 50 55 60
 Ile Ala Arg Asp Ser Cys Ala Val Phe Ala Trp Lys Arg Gly Thr Arg
 65 70 75 80
 Gln Glu Tyr Trp Cys Ser Thr Glu Pro Thr Leu Asp Trp Gly Pro Gly
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 Gly Gly Pro Asp Phe Asp Cys Asp Asp Gly Gly Asp Asp Pro Leu Leu

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Val	Pro	Asp	Pro	Ser	Cys	Thr	Asp	Asn	Ala	Glu	Phe	Gln	Val	Val	Leu
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Ile	Ile	Ile	Arg	Glu	Gly	Leu	Lys	Thr	Asp	Pro	Leu	Lys	Tyr	Thr	Lys
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Arg	Pro	Ser	Cys	Leu	Val	Gly	Val	Ser	Glu	Glu	Thr	Thr	Thr	Gly	Val
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Lys	Arg	Ser	Tyr	Gln	Met	Gln	Pro	Lys	Cys	Thr	Leu	Leu	Leu	His	Ala
			180					185					190		
Thr	Asp	Val	Cys	Asp	Thr	Val	Ile	Lys	Ser	Lys	Ile	Asp	Asn	Leu	Tyr
	195						200					205			
Gly	Cys	Arg	His	Ser	Leu	Ser	Asp	Gly	Leu	Met	Arg	Ala	Thr	Asp	Val
	210					215					220				
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	225				230					235					240
Lys	Gly	Trp	Val	Ala	Ala	Leu	Lys	Gln	Ala	Gly	Ala	Arg	Val	Ile	Val
				245					250					255	
Thr	Glu	Ile	Pro	Gln	Ile	Cys	Ala	Val	Gln	Ala	Thr	Met	Glu	Gly	Ser
			260					265					270		
Ser	Val	Leu	Thr	Leu	Glu	Asp	Val	Val	Ser	Asp	Val	Asp	Arg	Phe	Val
		275					280					285			
Thr	Thr	Thr	Gly	Asn	Lys	Asp	Leu	Ile	Met	Val	Asp	His	Met	Arg	Arg
	290					295					300				
Met	Lys	Asn	Gln	Ala	Ile	Val	Cys	Asn	Ile	Arg	Arg	Phe	Asp	Asn	Glu
	305				310					315					320
Ile	Asp	Met	Arg	Ser	Leu	Glu	Thr	Phe	Pro	Gly	Val	Lys	Arg	Ile	Thr
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Ile	Lys	Ala	Gln	Thr	Asp	Arg	Trp	Val	Phe	Arg	Asp	Thr	Asn	Arg	Gly
			340					345					350		
Ile	Ile	Val	Pro	Ala	Glu	Gly	Arg	Leu	Met	Thr	Met	Gly	Cys	Ala	Thr
		355					360					365			
Gly	His	Pro	Ser	Phe	Arg	Thr	Ser	Cys	Ser	Phe	Thr	Asn	Gln	Val	Ser
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Ser	Gln	Leu	Glu	Leu	Trp	Arg	Glu	Lys	Ser	Thr	Gly	Lys	Tyr	Glu	Lys
	385				390					395					400
Lys	Val	Tyr	Val	Phe	Pro	Lys	His	Leu	Glu	Lys	Lys	Val	Ala	Ala	Leu

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Asp Val Asp Glu Ile Val Arg Leu Arg Lys Arg Phe Phe Lys Leu Asp			
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aga gat tgt tca gga tca gaa ctt gga agt gag ttc atg agt ttg cct			144
Arg Asp Cys Ser Gly Ser Glu Leu Gly Ser Glu Phe Met Ser Leu Pro			
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caa gtt agt tcg aac cct ctt cgg atg cgt gag atg cgt aat ttc gat			192
Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp			
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Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg			
65	70	75	80
tcc agt ttc agt act gtc ggg cag aag aat gct aaa ttg aga ttt gca			288
Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala			
85	90	95	
ccg att atc tat gat tgc gat aaa gat gga cct ata tca aac ggt gag			336
Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu			
100	105	110	
tta ttt agg gtg ttg cgt att atg gtt cat gac aat ctg agt gat aat			384
Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn			
115	120	125	
cag ctg cag cag cgt tgc gat tgc acg cgt agt ggc gga gat aat gac			432
Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp			

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ttg cca gct acc gta cgt cgg cgt ccg tac cgt acg ttg gta agc ggt 528
Leu Pro Ala Thr Val Arg Arg Arg Pro Tyr Arg Thr Leu Val Ser Gly
165              170              175

gat gtg taa agttcagtgc accgtgaccg tgagcctgga agcctgaacg 577
Asp Val

ctgacaagcc cttagccaa aaaattggct gaggcctgat gccctgagat gccaaaggct 637

ttttaggctt ttagagaaaa aggctaaaaa aaaggctaga aaaaaaggct cttaggcctg 697

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35 40 45

Gln Val Ser Ser Asn Pro Leu Arg Met Arg Glu Met Arg Asn Phe Asp
50 55 60

Asn Asp Cys Val Gly Ser Val Asp Phe Ile Glu Phe Ile Asn Gly Arg
65 70 75 80

Ser Ser Phe Ser Thr Val Gly Gln Lys Asn Ala Lys Leu Arg Phe Ala
85 90 95

Pro Ile Ile Tyr Asp Cys Asp Lys Asp Gly Pro Ile Ser Asn Gly Glu
100 105 110

Leu Phe Arg Val Leu Arg Ile Met Val His Asp Asn Leu Ser Asp Asn
115 120 125

Gln Leu Gln Gln Arg Cys Asp Cys Thr Arg Ser Gly Gly Asp Asn Asp
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Gly Asp Gly Arg Gly Ala Lys Asn Ser Phe Glu Glu Phe Tyr Gly Arg
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Asp Val

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tgg gcg gtg aac ccc tgc ttc att gct tcc tgt tcc tgt ctc ctc gtt 99
Trp Ala Val Asn Pro Cys Phe Ile Ala Ser Cys Ser Cys Leu Leu Val
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ggc ttc ggc gac gca atc ttc tac gag tgc ttc gcc ggg gat ttt gat 147
Gly Phe Gly Asp Ala Ile Phe Tyr Glu Ser Phe Ala Gly Asp Phe Asp
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Ala Arg Trp Ile Leu Ser Gly Ser Lys Cys Leu Ser Asp Ser Ala Lys
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Asn Ala Gly Phe Asp Asp Tyr Gly Leu Leu Val Gly Glu Gln Ala Arg
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Lys Pro Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp
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gga aga gtt gtt ctt gag tgt gag act cgc ctt gac cat ggc atc gac 339
Gly Arg Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp
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Cys Gly Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp
          115             120             125

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Lys Phe Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg
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agg acc cag ttc ttc ggg ggc cac ccc cag aac cca aac agt ggt gag 483
Arg Thr Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu
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Val Pro Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln	
175 180 185 190	
atc ttg ata gat cgg ggg ttg gag acc aag gcc aaa atc ttc cct tgt	627
Ile Leu Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys	
195 200 205	
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Glu Asp Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn	
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Pro Ser Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly	
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cca agt gcc ctg aag cga cag gaa agc gat gag gat ccg aac cgg gaa	771
Pro Ser Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu	
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atc tta cat gaa gaa gcc ggg aga cgt tcg tcc gat gtt ggg gcc cac	819
Ile Leu His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His	
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Ala Lys Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu	
275 280 285	
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Lys Asp Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly	
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Ala Ala Pro Ser Cys Gly Val Ser Glu Arg Gln Thr Lys Ile Ser Pro	
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aat tat aag gga aaa ccc tcc gtg ggt cca aac gtt tac caa ggg att	1011
Asn Tyr Lys Gly Lys Pro Ser Val Gly Pro Asn Val Tyr Gln Gly Ile	
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Trp Lys Pro Arg Glu Met Leu Asn Pro Gly Ser Phe Gln Ile Ala Lys	
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ccc gct tgt gag cct att gct ggt ata ggc atg gag att agg aag cag	1107
Pro Ala Cys Glu Pro Ile Ala Gly Ile Gly Met Glu Ile Arg Lys Gln	
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Gly Ile Leu Leu Asp Thr Val Val Gly Val Arg Gly Asp Thr Gly Glu	
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 Glu Tyr Gly Glu Thr Pro Leu Lys Thr Thr Cys Thr Val Glu Lys His
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 Ser Leu Gln Ala Gln Glu Ala Arg Thr Arg Ser Asp Ala Gly Ser Pro
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 Tyr Thr Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe
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 Gln Cys Ala Asn Ala Val Ile Leu Gly Val Val Val Asn Ser Gly Ser
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 480 485 490
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 Gly Thr Gln Asp Arg Arg Lys Gln Asp Val Gly Arg Arg Gln Ala Ala
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 Pro Ile Val Lys Glu Leu Ala Glu Ser Leu Ser Leu Lys Asp Gly Arg
 85 90 95
 Val Val Leu Glu Cys Glu Thr Arg Leu Asp His Gly Ile Asp Cys Gly
 100 105 110
 Gly Pro Cys Ile Arg Tyr Leu Arg Thr Gln Glu Ser Gly Trp Lys Phe
 115 120 125
 Asp Ser Ser Thr Met Phe Gly Ala Ala Lys Tyr Gly Ala Arg Arg Thr
 130 135 140
 Gln Phe Phe Gly Gly His Pro Gln Asn Pro Asn Ser Gly Glu Cys Val
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 Asp His Asp His Asn Gln Arg Ala Ser Leu Thr Ser Asp Lys Val Pro
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 Arg Leu Tyr Thr Gly Ile Leu Ser Pro Glu Asn Glu Phe Gln Ile Leu
 180 185 190
 Ile Asp Arg Gly Leu Glu Thr Lys Ala Lys Ile Phe Pro Cys Glu Asp
 195 200 205
 Phe Glu Pro Pro Val Ile Pro Ser Lys Arg Ser Pro Asp Asn Pro Ser
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 Lys Arg Thr Glu Asp Ser Asp Glu Lys Ala Lys Ile Pro Gly Pro Ser
 225 230 235 240
 Ala Leu Lys Arg Gln Glu Ser Asp Glu Asp Pro Asn Arg Glu Ile Leu
 245 250 255
 His Glu Glu Ala Gly Arg Arg Ser Ser Asp Val Gly Ala His Ala Lys
 260 265 270
 Asp Gln Ala His Glu Pro Glu Pro Lys His Trp Gly Ala Glu Lys Asp
 275 280 285
 Gly Glu Cys Ala Pro Pro Lys Ile Glu Asn Ala Lys Arg Gly Ala Ala
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 Arg Tyr Val Ser Lys Ile Pro Gly Lys Ala Asp Asn Pro Phe Ser Ser
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 465 470 475 480
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 Arg Val Thr Arg Asp Gly Ser Gly Pro Gly Lys Thr Gly Val Thr Arg
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 Gly Ser Ser Pro Met Arg Trp Ala Trp Lys Arg Trp Gln Ala Val Gly
 30 35 40 45

gca tgc acg gcc cgc acg tgg ttc ggg aca gag aac cag aaa gga ata 195
 Ala Ser Thr Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile
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Thr	Thr	Ser	Thr	Arg	Ala	Arg	Arg	Tyr	Ala	Val	Ser	Ala	Lys	Phe	Pro	
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Arg	Leu	Ser	Asn	Lys	Gly	Lys	Asp	Tyr	Met	Arg	Cys	Val	Leu	Gln	Tyr	
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acc	gtc	aaa	aat	gaa	caa	aaa	gtt	gat	tgt	ggg	ggc	tca	tat	atc	aag	339
Thr	Val	Lys	Asn	Glu	Gln	Lys	Val	Asp	Cys	Gly	Gly	Ser	Tyr	Ile	Lys	
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tta	tta	cct	tcg	aaa	ttg	cgc	acg	ggg	gat	ggg	gat	ggc	gtg	tca	gaa	387
Leu	Leu	Pro	Ser	Lys	Leu	Arg	Thr	Gly	Asp	Gly	Asp	Gly	Val	Ser	Glu	
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Tyr	Ser	Ile	Met	Phe	Gly	Pro	Asp	Ser	Thr	Gly	Ala	Ser	Arg	Thr	Val	
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cgt	cga	gct	cgc	aat	tat	aag	ggg	aaa	cgg	cat	ttg	cgg	aaa	aaa	gaa	483
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Gln	Asn	Lys	Val	Glu	Thr	Asp	Gln	Leu	Thr	His	Gln	Tyr	Thr	Thr	Ser	
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Trp	Ser	Pro	Asp	Trp	Thr	Tyr	Asn	Val	Leu	Val	Asp	Asn	Lys	Glu	Ser	
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Ile	Phe	Arg	Pro	Ser	Cys	Arg	Lys	Gln	Ser	Lys	Pro	Val	Thr	Cys	Val	
				210				215						220		
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Asp	Val	Lys	His	His	Ala	Pro	Arg	Arg	Asn	Val	Lys	Pro	Ala	Gly	His	
			225					230					235			
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Asp	Asp	Ile	Pro	Ala	Arg	Arg	Thr	Thr	Pro	Glu	Ala	Val	Arg	Lys	Gly	
		240					245					250				
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Arg	Thr	Asn	Glu	Arg	Pro	Asp	Arg	Thr	Trp	Ala	Thr	Gly	Thr	Thr	Pro	
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cca gcc ccc ccg aac gac cta tat cta ttc ttg gac ctg ggt gca gca 963
 Pro Ala Pro Pro Asn Asp Leu Tyr Leu Phe Leu Asp Leu Gly Ala Ala
 305 310 315

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 Thr Gly Ile Gly Ala Glu Arg His Cys Ala Asp Glu Arg Trp Lys Glu
 370 375 380

aca acg gta gcc ccc gat tgc gcc gta tcg gca gcg aac gcc tcg cga 1203
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 385 390 395

cgc acc ggg gag ctg gcc acc ccg gtg acg atg ctg cct gat ccg ttg 1251
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 35 40 45

Ala Arg Thr Trp Phe Gly Thr Glu Asn Gln Lys Gly Ile Thr Thr Ser
 50 55 60

Thr Arg Ala Arg Arg Tyr Ala Val Ser Ala Lys Phe Pro Arg Leu Ser
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Asn Lys Gly Lys Asp Tyr Met Arg Cys Val Leu Gln Tyr Thr Val Lys
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 Asn Glu Gln Lys Val Asp Cys Gly Gly Ser Tyr Ile Lys Leu Leu Pro
 100 105 110
 Ser Lys Leu Arg Thr Gly Asp Gly Asp Gly Val Ser Glu Tyr Ser Ile
 115 120 125
 Met Phe Gly Pro Asp Ser Thr Gly Ala Ser Arg Thr Val Arg Arg Ala
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 Arg Asn Tyr Lys Gly Lys Arg His Leu Arg Lys Lys Glu Gln Asn Lys
 145 150 155 160
 Val Glu Thr Asp Gln Leu Thr His Gln Tyr Thr Thr Ser Trp Ser Pro
 165 170 175
 Asp Trp Thr Tyr Asn Val Leu Val Asp Asn Lys Glu Ser Gln Ala Gly
 180 185 190
 Asn Leu Ala Asp Asp Cys Glu Leu Leu Pro Gln Lys Arg Ile Phe Arg
 195 200 205
 Pro Ser Cys Arg Lys Gln Ser Lys Pro Val Thr Cys Val Asp Val Lys
 210 215 220
 His His Ala Pro Arg Arg Asn Val Lys Pro Ala Gly His Asp Asp Ile
 225 230 235 240
 Pro Ala Arg Arg Thr Thr Pro Glu Ala Val Arg Lys Gly Arg Thr Asn
 245 250 255
 Glu Arg Pro Asp Arg Thr Trp Ala Thr Gly Thr Thr Pro Arg Pro Arg
 260 265 270
 Arg Tyr Lys Gly Glu Thr Lys Ala Lys Lys His Pro Arg Pro Glu Tyr
 275 280 285
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Ile	Pro	Leu	Ile	Asp	Arg	Phe	Gln	Val	Glu	Ala	Phe	Leu	Arg	Leu	Met
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Gln	Lys	Gln	Ile	Gln	Ser	Ala	Gly	Lys	Arg	Gly	Phe	Phe	Tyr	Ser	Lys
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Lys	Ser	Ser	Gly	Ser	Asn	Val	Arg	Glu	Arg	Phe	Thr	Phe	Glu	Asp	Met
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Val	Ala	His	Asp	Ala	Thr	Ile	Glu	Pro	Asp	Ala	Gln	Val	Leu	Ala	Val
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Ile	Lys	Leu	Ser	Ala	Phe	Ser	Ser	Phe	Ser	Leu	Phe	Glu	Cys	Arg	Lys
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Ile	Leu	Lys	Ala	Leu	Pro	Tyr	Gly	Asn	Ser	Val	Phe	Phe	Ser	Val	Arg	
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Lys	Ile	Asp	Asp	Pro	Ile	Gly	Leu	Leu	Pro	Gly	Arg	Ile	Ile	Leu	Gly	
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Ile	Asn	Lys	Arg	Gly	Val	His	Phe	Phe	Arg	Pro	Val	Pro	Lys	Glu	Tyr	
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Thr	Ala	Val	Phe	Phe	Lys	Met	Arg	Val	Ala	Gly	Val	Leu	His	Ile	Phe	
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Gln	Phe	Glu	Thr	Lys	Gln	Gly	Glu	Glu	Ile	Cys	Val	Ala	Leu	Gln	Thr	
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Glu	Glu	Ser	Gln	Lys	Lys	Ile	Glu	Lys	Leu	Met	Asp	Glu	Gln	Gln	Glu	

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Glu	Val	Glu	Ile	His	Gln	Lys	Arg	Tyr	Glu	Gln	Glu	Lys	Lys	Val	Leu				
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 980 985 990
 Ser Asn Pro Gly Leu Thr Pro Arg Ala Thr Lys Glu Leu Phe Asn Ile
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 Ser Phe Val Asp Leu Ala Gly Ser Glu Arg Val Lys Lys Ser Gly Ser
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 Ala Gly Cys Gln Leu Lys Glu Ala Gln Ser Ile Asn Lys Ser Leu Ser
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 Pro Tyr Arg Asn His Lys Leu Thr Met Leu Met Ser Asp Ser Leu Gly
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 Gly Asn Ala Lys Thr Leu Met Phe Val Asn Val Ser Pro Ala Glu Ser
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Asn Asn Asn Pro Lys Ser His Asn Ser His Asn Ser Asn Gly Met Thr	
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ggg aac agg aac aat aat aat aaa aat gcc ggc gga gtt gaa act agt	192
Gly Asn Arg Asn Asn Asn Asn Lys Asn Ala Gly Gly Val Glu Thr Ser	
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Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn	
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Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr	
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gtt gac gta cca gtc ata tta agt acc cgg gaa tca caa ggc aca cgt	336
Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg	
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tca gta aat gca aca agt aaa att aga tgc ccg gat tcc act gca att	384
Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile	
115 120 125	
tgc gag tgg ttc gcc acg ccc acg gat cct caa aga cca gga gtt tat	432
Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr	
130 135 140	
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Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn	
145 150 155 160	

acc gtt agc agt cta atg gat aat gct agg ggt ccg aac ccg cga tct	528
Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser	
165 170 175	
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Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr	
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cct cca gat cca ctg cag aat cct aat aat tat act agg tat cat aat	624
Pro Pro Asp Pro Leu Gln Asn Pro Asn Asn Tyr Thr Arg Tyr His Asn	
195 200 205	
gat aaa aac agc aag aat agt aac aga aac tac aat aag aga aat aag	672
Asp Lys Asn Ser Lys Asn Ser Asn Arg Asn Tyr Asn Lys Arg Asn Lys	
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Asn Ser Thr Thr Phe Asn Asn Ser Asp Leu Pro Gly His Asn Arg Ser	
225 230 235 240	
tcc cct gcg att aat gca gta aaa tca gca tca aat cga tca tct gct	768
Ser Pro Ala Ile Asn Ala Val Lys Ser Ala Ser Asn Arg Ser Ser Ala	
245 250 255	
ata ggt agt cga aac agt gat tta aac aat gct gct aat gat gaa cgc	816
Ile Gly Ser Arg Asn Ser Asp Leu Asn Asn Ala Ala Asn Asp Glu Arg	
260 265 270	
cat tac gct aga tcg gga aca tat cag ata aac gct gta aca gta ctt	864
His Tyr Ala Arg Ser Gly Thr Tyr Gln Ile Asn Ala Val Thr Val Leu	
275 280 285	
aga gta tta gga aga gga gca cgg cgt gat gta aag tca gca tat cat	912
Arg Val Leu Gly Arg Gly Ala Arg Arg Asp Val Lys Ser Ala Tyr His	
290 295 300	
ggc acc tgt ggt aca ggt ccc cgg atg aaa gtg ata aca ttg gct gtt	960
Gly Thr Cys Gly Thr Gly Pro Arg Met Lys Val Ile Thr Leu Ala Val	
305 310 315 320	
caa gag aat att aga aac cga att ata ttg gag cta cgg aca tta cac	1008
Gln Glu Asn Ile Arg Asn Arg Ile Ile Leu Glu Leu Arg Thr Leu His	
325 330 335	
aag acc tct tat caa tat atc gtt ccg tat tat gat ggg atc tat aca	1056
Lys Thr Ser Tyr Gln Tyr Ile Val Pro Tyr Tyr Asp Gly Ile Tyr Thr	
340 345 350	
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Glu Gly Ser Ile Phe Ile Arg Met Val Glu Leu Gly Trp Val Thr Asn	
355 360 365	
atc atg aac aaa acg gcg acc ata cgt gcg ccg gtt ttg ggt acg atg	1152
Ile Met Asn Lys Thr Ala Thr Ile Arg Ala Pro Val Leu Gly Thr Met	
370 375 380	
gca ttt cta gtg tta caa ggt cgg att tac gtt cac aga aag ttc gat	1200

Ala Phe Leu Val Leu Gln Gly Arg Ile Tyr Val His Arg Lys Phe Asp 385 390 395 400	
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aat gaa ggt cga gca aag atc gca ggt ttc ggt gta agc gga cag tta Asn Glu Gly Arg Ala Lys Ile Ala Gly Phe Gly Val Ser Gly Gln Leu 420 425 430	1296
caa cat act ctc tca aag gat gta act tcg gtg gag tct cct gaa cgt Gln His Thr Leu Ser Lys Asp Val Thr Ser Val Glu Ser Pro Glu Arg 435 440 445	1344
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ata aca cgt gta tca tgc gca atc ggg aga ttc cct tat gct tgt aat Ile Thr Arg Val Ser Cys Ala Ile Gly Arg Phe Pro Tyr Ala Cys Asn 465 470 475 480	1440
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agt aac aat cct aat aat agg aat gat aat aat aac act gta tgc gat Ser Asn Asn Pro Asn Asn Arg Asn Asp Asn Asn Asn Thr Val Cys Asp 545 550 555 560	1680
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610 615 620
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 Lys Lys Ala Arg Ser Arg Leu Glu Thr His Pro Arg Asp Asn Glu Asn
 65 70 75 80
 Asn Tyr Arg Leu Ala Thr Ser Ala Gly Thr Lys Gly Gly Ala Arg Thr
 85 90 95
 Val Asp Val Pro Val Ile Leu Ser Thr Arg Glu Ser Gln Gly Thr Arg
 100 105 110
 Ser Val Asn Ala Thr Ser Lys Ile Arg Cys Pro Asp Ser Thr Ala Ile
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 Cys Glu Trp Phe Ala Thr Pro Thr Asp Pro Gln Arg Pro Gly Val Tyr
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 Asn His Lys Asn Gly Asp Lys Asn Asn Arg Asp Thr Gly Asn Ile Asn
 145 150 155 160
 Thr Val Ser Ser Leu Met Asp Asn Ala Arg Gly Pro Asn Pro Arg Ser
 165 170 175
 Gly Ile Ser Ile Pro Thr Pro Thr Ser Arg Gln Ser Pro Ser Glu Thr

179

Pro	Ala	Asp	Ser	Arg	Lys	Leu	Val	Ala	Asn	Ser	Thr	Ser	Phe	His	Pro	
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Ile	Ser	Ala	Val	Asn	Val	Ser	Ala	Gln	Ala	Ser	Leu	Thr	Ala	Asp	Phe	
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ccc	gcc	ctt	tca	gaa	act	ata	ctg	aaa	gag	gga	aga	aat	aac	gga	aaa	292
Pro	Ala	Leu	Ser	Glu	Thr	Ile	Leu	Lys	Glu	Gly	Arg	Asn	Asn	Gly	Lys	
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gag	aaa	gca	gag	aac	atc	gtg	tgg	cac	gag	agt	tcg	ata	tgc	aga	tgc	340
Glu	Lys	Ala	Glu	Asn	Ile	Val	Trp	His	Glu	Ser	Ser	Ile	Cys	Arg	Cys	
	90				95					100					105	
gac	aga	caa	caa	ctt	ctt	caa	caa	aag	ggt	tgt	gtc	gtt	tgg	atc	act	388
Asp	Arg	Gln	Gln	Leu	Leu	Gln	Gln	Lys	Gly	Cys	Val	Val	Trp	Ile	Thr	
				110					115					120		
ggt	ctc	agt	ggt	tca	ggg	aaa	agc	act	gtt	gct	tgt	gca	cta	agt	aaa	436
Gly	Leu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Val	Ala	Cys	Ala	Leu	Ser	Lys	
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Ala	Leu	Phe	Glu	Arg	Gly	Lys	Leu	Thr	Tyr	Thr	Leu	Asp	Gly	Asp	Asn	
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Val	Arg	His	Gly	Leu	Asn	Arg	Asp	Leu	Thr	Phe	Lys	Ala	Glu	His	Arg	
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Thr	Glu	Asn	Ile	Arg	Arg	Ile	Gly	Glu	Val	Ala	Lys	Leu	Phe	Ala	Asp	
	170				175					180					185	
gtc	gga	gtc	att	tgt	ata	gca	agt	ttg	att	tct	ccg	tac	cgg	aga	gac	628
Val	Gly	Val	Ile	Cys	Ile	Ala	Ser	Leu	Ile	Ser	Pro	Tyr	Arg	Arg	Asp	
				190					195					200		
aga	gac	gcg	tgc	cgg	tcc	ttg	tta	cct	gac	ggc	gat	ttc	gtc	gag	gtc	676
Arg	Asp	Ala	Cys	Arg	Ser	Leu	Leu	Pro	Asp	Gly	Asp	Phe	Val	Glu	Val	
			205					210					215			
ttc	atg	gac	gtt	cct	ctt	cat	gtg	tgc	gag	tcg	aga	gat	cca	aag	ggg	724
Phe	Met	Asp	Val	Pro	Leu	His	Val	Cys	Glu	Ser	Arg	Asp	Pro	Lys	Gly	
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ttg	tac	aag	ctt	gca	cgt	gca	ggc	aaa	atc	aaa	ggc	ttc	act	gga	atc	772
Leu	Tyr	Lys	Leu	Ala	Arg	Ala	Gly	Lys	Ile	Lys	Gly	Phe	Thr	Gly	Ile	
	235					240					245					
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Asp	Asp	Pro	Tyr	Glu	Ala	Pro	Val	Asn	Cys	Glu	Val	Val	Leu	Lys	His	
	250				255				260						265	
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Thr	Gly	Asp	Asp	Glu	Ser	Cys	Ser	Pro	Arg	Gln	Met	Ala	Glu	Asn	Ile	

270 275 280
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 Phe Leu Lys Leu Pro Ala Ser Ser Ile Pro Ala Asp Ser Arg Lys Leu
 35 40 45
 Val Ala Asn Ser Thr Ser Phe His Pro Ile Ser Ala Val Asn Val Ser
 50 55 60
 Ala Gln Ala Ser Leu Thr Ala Asp Phe Pro Ala Leu Ser Glu Thr Ile
 65 70 75 80
 Leu Lys Glu Gly Arg Asn Asn Gly Lys Glu Lys Ala Glu Asn Ile Val
 85 90 95
 Trp His Glu Ser Ser Ile Cys Arg Cys Asp Arg Gln Gln Leu Leu Gln
 100 105 110
 Gln Lys Gly Cys Val Val Trp Ile Thr Gly Leu Ser Gly Ser Gly Lys
 115 120 125
 Ser Thr Val Ala Cys Ala Leu Ser Lys Ala Leu Phe Glu Arg Gly Lys
 130 135 140
 Leu Thr Tyr Thr Leu Asp Gly Asp Asn Val Arg His Gly Leu Asn Arg
 145 150 155 160
 Asp Leu Thr Phe Lys Ala Glu His Arg Thr Glu Asn Ile Arg Arg Ile
 165 170 175
 Gly Glu Val Ala Lys Leu Phe Ala Asp Val Gly Val Ile Cys Ile Ala
 180 185 190
 Ser Leu Ile Ser Pro Tyr Arg Arg Asp Arg Asp Ala Cys Arg Ser Leu
 195 200 205
 Leu Pro Asp Gly Asp Phe Val Glu Val Phe Met Asp Val Pro Leu His
 210 215 220

Val Cys Glu Ser Arg Asp Pro Lys Gly Leu Tyr Lys Leu Ala Arg Ala
 225 230 235 240

Gly Lys Ile Lys Gly Phe Thr Gly Ile Asp Asp Pro Tyr Glu Ala Pro
 245 250 255

Val Asn Cys Glu Val Val Leu Lys His Thr Gly Asp Asp Glu Ser Cys
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Gly Tyr Leu Glu Gly
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 Ser Gly Ala Ser Thr Lys Tyr Asp Ala Lys Asp Ile Gly Ser Leu Gly
 15 20 25

agc aag gct tcg tct gtg tct gta aga cca agc cct cga act gag ggt 147
 Ser Lys Ala Ser Ser Val Ser Val Arg Pro Ser Pro Arg Thr Glu Gly
 30 35 40 45

gag atc tta cag tct cca aat ctc aag agt ttt agc ttt gct gag ctt 195
 Glu Ile Leu Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu
 50 55 60

aaa tca gca acc agg aat ttt aga cca gac agt gtg ctt ggt gaa ggt 243
 Lys Ser Ala Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly
 65 70 75

gga ttc ggt tgt gtt ttc aaa gga tgg att gat gag aag tct ctc act 291
 Gly Phe Gly Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr
 80 85 90

gcc tca aga cca ggc acg ggt ttg gtt att gcc gtc aaa aag ctt aac 339
 Ala Ser Arg Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn
 95 100 105

caa gat ggt tgg caa ggt cac cag gag tgg ctg gct gaa gtg aat tac 387
 Gln Asp Gly Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr

110	115	120	125	
ctt ggt cag ttt tct cac cgt cac ctt gtg aag ctg att ggt tat tgc				435
Leu Gly Gln Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys	130	135	140	
cta gag gat gag cac cgt ctt ctt gtt tac gag ttc atg cct cgg ggt				483
Leu Glu Asp Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly	145	150	155	
agc ttg gag aat cat ctt ttc agg aga ggt ttg tac ttc caa ccg tta				531
Ser Leu Glu Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu	160	165	170	
tct tgg aaa ctt cgg ttg aaa gtt gct ctt ggt gct gca aag gga ctt				579
Ser Trp Lys Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu	175	180	185	
gct ttt ctt cac agt tcc gag aca aga gtg ata tac cga gat ttc aag				627
Ala Phe Leu His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys	190	195	200	205
act tct aat atc ctt ctt gac tcg gag tac aac gca aag ctt tct gat				675
Thr Ser Asn Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp	210	215	220	
ttt ggg ttg gct aag gat ggg cca ata ggt gat aaa agt cat gtc tct				723
Phe Gly Leu Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser	225	230	235	
aca cga gtc atg ggt aca cac gga tat gca gct cct gaa tac ctt gca				771
Thr Arg Val Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala	240	245	250	
acc ggt cat cta aca aca aag agt gat gtc tat agc ttc ggg gtt gtc				819
Thr Gly His Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val	255	260	265	
ctt ctg gag ctg ttg tct ggt cgt cga gca gtg gac aag aac cgc cca				867
Leu Leu Glu Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro	270	275	280	285
tct gga gag agg aac ctt gtg gag tgg gct aaa cca tac ctc gta aac				915
Ser Gly Glu Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn	290	295	300	
aaa aga aag ata ttc cga gtc att gat aat cgt ctt cag gac cag tac				963
Lys Arg Lys Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr	305	310	315	
tct atg gaa gaa gca tgt aaa gtg gct act ctg tct ctg aga tgt ctc				1011
Ser Met Glu Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu	320	325	330	
acc aca gag att aag ctg aga cca aac atg agc gag gtt gtt tcg cac				1059
Thr Thr Glu Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His	335	340	345	

ctc gaa cac att cag tct tta aat gct gct ata gga gga aat atg gat 1107
 Leu Glu His Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp
 350 355 360 365

aaa aca gat aga aga atg cgt agg aga agt gac agt gtt gtc agc aaa 1155
 Lys Thr Asp Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys
 370 375 380

aaa gtg aat gca ggt ttt gct cga cag act gct gtt ggc agt aca gtt 1203
 Lys Val Asn Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val
 385 390 395

gtt gct tat cct cgc cca tca gcc tcg cca ctg tat gtt tga 1245
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 35 40 45

Gln Ser Pro Asn Leu Lys Ser Phe Ser Phe Ala Glu Leu Lys Ser Ala
 50 55 60

Thr Arg Asn Phe Arg Pro Asp Ser Val Leu Gly Glu Gly Gly Phe Gly
 65 70 75 80

Cys Val Phe Lys Gly Trp Ile Asp Glu Lys Ser Leu Thr Ala Ser Arg
 85 90 95

Pro Gly Thr Gly Leu Val Ile Ala Val Lys Lys Leu Asn Gln Asp Gly
 100 105 110

Trp Gln Gly His Gln Glu Trp Leu Ala Glu Val Asn Tyr Leu Gly Gln
 115 120 125

Phe Ser His Arg His Leu Val Lys Leu Ile Gly Tyr Cys Leu Glu Asp
 130 135 140

Glu His Arg Leu Leu Val Tyr Glu Phe Met Pro Arg Gly Ser Leu Glu
 145 150 155 160

Asn His Leu Phe Arg Arg Gly Leu Tyr Phe Gln Pro Leu Ser Trp Lys

	165		170		175
Leu Arg Leu Lys Val Ala Leu Gly Ala Ala Lys Gly Leu Ala Phe Leu	180		185		190
His Ser Ser Glu Thr Arg Val Ile Tyr Arg Asp Phe Lys Thr Ser Asn	195		200		205
Ile Leu Leu Asp Ser Glu Tyr Asn Ala Lys Leu Ser Asp Phe Gly Leu	210		215		220
Ala Lys Asp Gly Pro Ile Gly Asp Lys Ser His Val Ser Thr Arg Val	225		230		235
Met Gly Thr His Gly Tyr Ala Ala Pro Glu Tyr Leu Ala Thr Gly His		245		250	255
Leu Thr Thr Lys Ser Asp Val Tyr Ser Phe Gly Val Val Leu Leu Glu		260		265	270
Leu Leu Ser Gly Arg Arg Ala Val Asp Lys Asn Arg Pro Ser Gly Glu		275		280	285
Arg Asn Leu Val Glu Trp Ala Lys Pro Tyr Leu Val Asn Lys Arg Lys		290		295	300
Ile Phe Arg Val Ile Asp Asn Arg Leu Gln Asp Gln Tyr Ser Met Glu		305		310	315
Glu Ala Cys Lys Val Ala Thr Leu Ser Leu Arg Cys Leu Thr Thr Glu		325		330	335
Ile Lys Leu Arg Pro Asn Met Ser Glu Val Val Ser His Leu Glu His		340		345	350
Ile Gln Ser Leu Asn Ala Ala Ile Gly Gly Asn Met Asp Lys Thr Asp		355		360	365
Arg Arg Met Arg Arg Arg Ser Asp Ser Val Val Ser Lys Lys Val Asn		370		375	380
Ala Gly Phe Ala Arg Gln Thr Ala Val Gly Ser Thr Val Val Ala Tyr		385		390	395
Pro Arg Pro Ser Ala Ser Pro Leu Tyr Val		405		410	

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 Met Leu Glu Lys Lys Leu Ala Ala Ala Glu Val Ser Glu Glu
 1 5 10

 gag caa aat aac ttg cta aag gat ttg gag atg aag gaa act gaa tat 158
 Glu Gln Asn Asn Leu Leu Lys Asp Leu Glu Met Lys Glu Thr Glu Tyr
 15 20 25 30

 atg cgc cgt cag agg cat aaa atg gga gct gat gac ttt gag cca ttg 206

148

Leu Asp Cys Ser Asn Leu Gln Glu Lys Asp Phe Thr Val Ala Arg Asn
 195 200 205
 gtt agt ggg gct tta caa agt gat ggt cgc cct gtg gcg aca aga cgc 1078
 Val Ser Gly Ala Leu Gln Ser Asp Gly Arg Pro Val Ala Thr Arg Arg
 210 215 220
 acc caa caa gag caa tta cta aac tgg cag aga aat aga agg atg ctt 1126
 Thr Gln Gln Glu Gln Leu Leu Asn Trp Gln Arg Asn Arg Arg Met Leu
 225 230 235
 gtaagtttca cttattcctc atcttttctt ccagagatgt ggagtagtcc acagtatcca 1186
 gtatatttcg ttattgaaag caaattctct ccattgatat agacatctat gttagatatg 1246
 acttactagg ttaaggtcat tacttttcag gct tat tcc aca gtt ggc act cct 1299
 Ala Tyr Ser Thr Val Gly Thr Pro
 240 245
 gac tat att gcc cca gaa gtt ctg ttg aaa aaa gga tat gga atg gaa 1347
 Asp Tyr Ile Ala Pro Glu Val Leu Leu Lys Lys Gly Tyr Gly Met Glu
 250 255 260
 tgt gat tg gtaggtgaag ccaacctatt cctatttgtg gtcttttgatt tctttggtgt 1405
 Cys Asp Tr
 265
 aaataaataa tatgggtgaa taatcttgag atttag g tgg tct ctt ggc gcc att 1460
 p Trp Ser Leu Gly Ala Ile
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 atg tat gaa atg ctt gtg ggg ttt ccg ccc ttt tat tca gat gac cca 1508
 Met Tyr Glu Met Leu Val Gly Phe Pro Pro Phe Tyr Ser Asp Asp Pro
 275 280 285
 atg aca act tgt agg aag gtaattaatc cattcctttt tgaatctttc 1556
 Met Thr Thr Cys Arg Lys
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 tatctctttg gtaattctaa tgtggaaact tacctcttct cgattcatta tcttccccct 1676
 tatgcag ata gta aat tgg aga aat tac ttg aaa ttc cca gat gag gtt 1725
 Ile Val Asn Trp Arg Asn Tyr Leu Lys Phe Pro Asp Glu Val
 295 300 305
 aga cta tca cca gaa gcc aag gat ctt att tgt agg ctt tta tgc aat 1773
 Arg Leu Ser Pro Glu Ala Lys Asp Leu Ile Cys Arg Leu Leu Cys Asn
 310 315 320
 gtt gaa caa agg ctt gga aca aaa gga gca gat gaa att aag 1815
 Val Glu Gln Arg Leu Gly Thr Lys Gly Ala Asp Glu Ile Lys
 325 330 335
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150

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Arg Gln Arg His Lys Met Gly Ala Asp Asp Phe Glu Pro Leu Thr Met
          35          40          45
Ile Gly Lys Gly Ala Phe Gly Glu Val Arg Ile Cys Arg Glu Lys Gly
  50          55          60
Thr Gly Asn Val Tyr Ala Met Lys Lys Leu Lys Lys Ser Glu Met Leu
  65          70          75          80
Arg Arg Gly Gln Val Val Glu His Val Lys Ala Glu Arg Asn Leu Leu
          85          90          95
Ala Glu Val Asp Ser Asn Cys Ile Val Lys Leu Tyr Cys Ser Phe Gln
          100          105          110
Asp Glu Glu Tyr Leu Tyr Leu Ile Met Glu Tyr Leu Pro Gly Gly Asp
  115          120          125
Met Met Thr Leu Leu Met Arg Lys Asp Thr Leu Thr Glu Asp Glu Ala
  130          135          140
Arg Phe Tyr Ile Gly Glu Thr Val Leu Ala Ile Glu Ser Ile His Lys
  145          150          155          160
His Asn Tyr Ile His Arg Asp Ile Lys Pro Asp Asn Leu Leu Leu Asp
          165          170          175
Lys Asp Gly His Met Lys Leu Ser Asp Phe Gly Leu Cys Lys Pro Leu

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180					185					190					
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Ser	Gly	Ala	Leu	Gln	Ser	Asp	Gly	Arg	Pro	Val	Ala	Thr	Arg	Arg	Thr
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Gln	Gln	Glu	Gln	Leu	Leu	Asn	Trp	Gln	Arg	Asn	Arg	Arg	Met	Leu	Ala
225					230					235					240
Tyr	Ser	Thr	Val	Gly	Thr	Pro	Asp	Tyr	Ile	Ala	Pro	Glu	Val	Leu	Leu
				245					250					255	
Lys	Lys	Gly	Tyr	Gly	Met	Glu	Cys	Asp	Trp	Trp	Ser	Leu	Gly	Ala	Ile
			260					265					270		
Met	Tyr	Glu	Met	Leu	Val	Gly	Phe	Pro	Pro	Phe	Tyr	Ser	Asp	Asp	Pro
		275					280						285		
Met	Thr	Thr	Cys	Arg	Lys	Ile	Val	Asn	Trp	Arg	Asn	Tyr	Leu	Lys	Phe
	290					295					300				
Pro	Asp	Glu	Val	Arg	Leu	Ser	Pro	Glu	Ala	Lys	Asp	Leu	Ile	Cys	Arg
305					310					315					320
Leu	Leu	Cys	Asn	Val	Glu	Gln	Arg	Leu	Gly	Thr	Lys	Gly	Ala	Asp	Glu
				325					330					335	
Ile	Lys	Gly	His	Pro	Trp	Phe	Arg	Gly	Thr	Glu	Trp	Gly	Lys	Leu	Tyr
			340					345					350		
Gln	Met	Lys	Ala	Ala	Phe	Ile	Pro	Gln	Val	Asn	Asp	Glu	Leu	Asp	Thr
		355					360					365			
Gln	Asn	Phe	Glu	Lys	Phe	Glu	Glu	Thr	Asp	Lys	Gln	Val	Pro	Lys	Ser
	370					375					380				
Ala	Lys	Ser	Gly	Pro	Trp	Arg	Lys	Met	Leu	Ser	Ser	Lys	Asp	Ile	Asn
385					390					395					400
Phe	Val	Gly	Tyr	Thr	Tyr	Lys	Asn	Val	Glu	Ile	Val	Asn	Asp	Asp	Gln
				405					410					415	
Ile	Pro	Gly	Ile	Ala	Glu	Leu	Lys	Lys	Lys	Ser	Asn	Lys	Pro	Lys	Arg
			420				425						430		
Pro	Ser	Ile	Lys	Ser	Leu	Phe	Glu	Asp	Glu	Thr	Ser	Gly	Gly	Thr	Thr
		435					440					445			
Thr	His	Gln	Gly	Ser	Phe	Leu	Asn	Leu	Leu	Pro	Thr	Gln	Ile	Glu	Asp
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Met Asn Gly Asp Glu Cys Ala Asn Val Ala Thr Cys Trp Val Thr Ser
 10           15           20           25

cta gct tgt gta gtt gac gcc gga cga tat acg aaa aag gta tcc cac 150
Leu Ala Cys Val Val Asp Ala Gly Arg Tyr Thr Lys Lys Val Ser His
           30           35           40

gac cgg cga acg agg tgg ccc gcc tgg aaa gca cga cgg gat cgt cat 198
Asp Arg Arg Thr Arg Trp Pro Ala Trp Lys Ala Arg Arg Asp Arg His
           45           50           55

agt gtc cga agt gat agc ggc cta gac agt cat gca ctt gaa ggt gga 246
Ser Val Arg Ser Asp Ser Gly Leu Asp Ser His Ala Leu Glu Gly Gly
           60           65           70

aaa cga cgt gag tca tgc gta tca cta gct cac gaa cga gat tat gca 294
Lys Arg Arg Glu Ser Cys Val Ser Leu Ala His Glu Arg Asp Tyr Ala
           75           80           85

cta acg gca cgg tgg gat cgt agc att gca atg acg gat gac acg aac 342
Leu Thr Ala Arg Trp Asp Arg Ser Ile Ala Met Thr Asp Asp Thr Asn
           90           95          100          105

cca caa acc caa cgt aaa ttt gag aaa cat act cgg gat gta gaa gct 390
Pro Gln Thr Gln Arg Lys Phe Glu Lys His Thr Arg Asp Val Glu Ala
           110          115          120

gtt cga ttt tct cca cga gat cgt cta att gta tct gcg ggt gca gat 438
Val Arg Phe Ser Pro Arg Asp Arg Leu Ile Val Ser Ala Gly Ala Asp
           125          130          135

ggg gta att gca gta tgt ccg gtt gct ggt gaa tgt gat gat gac gat 486
Gly Val Ile Ala Val Cys Pro Val Ala Gly Glu Cys Asp Asp Asp Asp
           140          145          150

gcc cgt gat ggt cat gaa gat tgt gtt agt agt att tgc ttt tca cca 534
Ala Arg Asp Gly His Glu Asp Cys Val Ser Ser Ile Cys Phe Ser Pro
           155          160          165

tca cta gaa cac ccg atc ctc ttt tct ggt agt tgt atc tac ttt att 582
Ser Leu Glu His Pro Ile Leu Phe Ser Gly Ser Cys Ile Tyr Phe Ile

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aaa gtg tgg aat gtc aat gga aag aaa tgt agg acg ccg cta aaa aag 630
Lys Val Trp Asn Val Asn Gly Lys Lys Cys Arg Thr Pro Leu Lys Lys
                      190                      195                      200

cat agt aat ccc gta tct aca cgg aca cag tca gaa gag gga agg cta 678
His Ser Asn Pro Val Ser Thr Arg Thr Gln Ser Glu Glu Gly Arg Leu
                      205                      210                      215

tgt gca aaa ggt ggt aaa agc ggt gca cgg cta cta ccc gat cta agt 726
Cys Ala Lys Gly Gly Lys Ser Gly Ala Arg Leu Leu Pro Asp Leu Ser
                      220                      225                      230

act cag gaa caa cta ccc aaa att aat caa gaa aac cct att aat caa 774
Thr Gln Glu Gln Leu Pro Lys Ile Asn Gln Glu Asn Pro Ile Asn Gln
                      235                      240                      245

att gct ttt tca cct agt ccg ttc gtc gtc acg tgc caa acg gaa aga 822
Ile Ala Phe Ser Pro Ser Pro Phe Val Val Thr Cys Gln Thr Glu Arg
250                      255                      260                      265

tcc cta tct caa acg tgg tga ccgtgcaccg gcacgggtgaa aaagtcgacc 873
Ser Leu Ser Gln Thr Trp
                      270

ggatcgaccg accgaaagcc tgctcgctgg acaaaaaaag agcttttttag gccttttcgct 933

ttttttgaag aaaaaaggct cgcgaaaaaa aaaaagctcg aatatca 979

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Asn Val Ala Thr Cys Trp Val Thr Ser Leu Ala Cys Val Val Asp Ala
          20           25           30

Gly Arg Tyr Thr Lys Lys Val Ser His Asp Arg Arg Thr Arg Trp Pro
          35           40           45

Ala Trp Lys Ala Arg Arg Asp Arg His Ser Val Arg Ser Asp Ser Gly
          50           55           60

Leu Asp Ser His Ala Leu Glu Gly Gly Lys Arg Arg Glu Ser Cys Val
          65           70           75           80

Ser Leu Ala His Glu Arg Asp Tyr Ala Leu Thr Ala Arg Trp Asp Arg
          85           90           95

Ser Ile Ala Met Thr Asp Asp Thr Asn Pro Gln Thr Gln Arg Lys Phe
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Met Lys Arg Leu Ser
1 5

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agc tca gat tca atg tgt ggt cta atc tcc act tct aca g gttcttatta 165
Ser Ser Asp Ser Met Cys Gly Leu Ile Ser Thr Ser Thr A
      10                      15

ccatctttgt tctttctact ttttgctaag gtcagacaaa acccatgtga tcctttcttc 225

actttccact gtttctttta ttgacaag at tca ttt ggt tac aca aca gat gaa 279
      sp Ser Phe Gly Tyr Thr Thr Asp Glu
      20                      25

cag agt cca aga ggg tac gga agt aat tac caa tct atg ctt gaa ggt 327
Gln Ser Pro Arg Gly Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly
      30                      35                      40

tac gat gaa gat gct aca cta atc gag gaa tat tcc ggc aac cac cac 375
Tyr Asp Glu Asp Ala Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His
      45                      50                      55

cac atg ggt cta tcg gag aag aag aga aga tta aaa gtt gac caa gtc 423
His Met Gly Leu Ser Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val
      60                      65                      70                      75

aaa gct ctt gag aag aat ttc gaa ctt gag aat aaa ctc gaa cct gag 471
Lys Ala Leu Glu Lys Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu
      80                      85                      90

agg aaa act aaa tta gca caa gag ctt gga ctt caa cct cgt caa gta 519
Arg Lys Thr Lys Leu Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val
      95                      100                      105

gct gtt tgg ttt cag aac cgt cgt gca cgg tgg aaa aca aaa cag ctt 567
Ala Val Trp Phe Gln Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu
      110                      115                      120

gaa aaa gat tac ggt gtt ctt aag ggt caa tac gat tct ctc cgc cac 615
Glu Lys Asp Tyr Gly Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His
      125                      130                      135

aat ttc gat tct ctc cgc cgt gac aat gat tcc ctt ctc caa gag 660
Asn Phe Asp Ser Leu Arg Asp Asn Asp Ser Leu Leu Gln Glu
      140                      145                      150

gtacaatatt agagacttta aaccataaaa attgaaactt cagagacgaa aatgcaaaaa 720

ggtttgattt ttaaagtttt tggttgcag att agt aaa atc aaa gct aag gta 773
      Ile Ser Lys Ile Lys Ala Lys Val
      155                      160

aac ggt gaa gaa gat aac aac aac aac aaa gct att acg gag ggt gtt 821
Asn Gly Glu Glu Asp Asn Asn Asn Asn Lys Ala Ile Thr Glu Gly Val
      165                      170                      175

aag gaa gag gaa gtt cac aag acg gat tcg att cct tcg tct cct ctg 869
Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser Pro Leu
      180                      185                      190

cag ttt cta gaa cat tcc tct ggt ttt aac tac cgg cga agc ttc act 917

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Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser Phe Thr
 195 200 205 210
 gac ctc cgt gac ctt cta ccg aat tcc acc gtt gtc gag gct gga tct 965
 Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala Gly Ser
 215 220 225
 tcc gat agt tgc gat tca agc gcc gtt ctt aac gac gaa aca agt tct 1013
 Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr Ser Ser
 230 235 240
 gat aac gga aga ttg acg ccg cct gtg acg gtt act ggc ggg agt ttc 1061
 Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly Ser Phe
 245 250 255
 tta cag ttt gtg aaa aca gag caa aca gag gat cac gag gat ttt cta 1109
 Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp Phe Leu
 260 265 270
 agc ggt gaa gaa gct tgt ggt ttc ttc tcc gat gaa cag ccg ccg tca 1157
 Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro Pro Ser
 275 280 285 290
 ctt cat tgg tac tct gct tca gat cat tgg act tga gaattgttta 1203
 Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
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<213> Arabidopsis thaliana

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 Tyr Gly Ser Asn Tyr Gln Ser Met Leu Glu Gly Tyr Asp Glu Asp Ala
 35 40 45
 Thr Leu Ile Glu Glu Tyr Ser Gly Asn His His His Met Gly Leu Ser
 50 55 60
 Glu Lys Lys Arg Arg Leu Lys Val Asp Gln Val Lys Ala Leu Glu Lys
 65 70 75 80
 Asn Phe Glu Leu Glu Asn Lys Leu Glu Pro Glu Arg Lys Thr Lys Leu
 85 90 95
 Ala Gln Glu Leu Gly Leu Gln Pro Arg Gln Val Ala Val Trp Phe Gln
 100 105 110

Asn Arg Arg Ala Arg Trp Lys Thr Lys Gln Leu Glu Lys Asp Tyr Gly
 115 120 125
 Val Leu Lys Gly Gln Tyr Asp Ser Leu Arg His Asn Phe Asp Ser Leu
 130 135 140
 Arg Arg Asp Asn Asp Ser Leu Leu Gln Glu Ile Ser Lys Ile Lys Ala
 145 150 155 160
 Lys Val Asn Gly Glu Glu Asp Asn Asn Asn Lys Ala Ile Thr Glu
 165 170 175
 Gly Val Lys Glu Glu Glu Val His Lys Thr Asp Ser Ile Pro Ser Ser
 180 185 190
 Pro Leu Gln Phe Leu Glu His Ser Ser Gly Phe Asn Tyr Arg Arg Ser
 195 200 205
 Phe Thr Asp Leu Arg Asp Leu Leu Pro Asn Ser Thr Val Val Glu Ala
 210 215 220
 Gly Ser Ser Asp Ser Cys Asp Ser Ser Ala Val Leu Asn Asp Glu Thr
 225 230 235 240
 Ser Ser Asp Asn Gly Arg Leu Thr Pro Pro Val Thr Val Thr Gly Gly
 245 250 255
 Ser Phe Leu Gln Phe Val Lys Thr Glu Gln Thr Glu Asp His Glu Asp
 260 265 270
 Phe Leu Ser Gly Glu Glu Ala Cys Gly Phe Phe Ser Asp Glu Gln Pro
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 Pro Ser Leu His Trp Tyr Ser Ala Ser Asp His Trp Thr
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 Ser Ser Ile Arg Trp Phe Ala Asn Arg Leu Val Ser Gly Ser Leu Leu
 15 20 25
 ttg tgt gct aac gcc tac agt cgt cgt act ccc gcg tcc ggg gcc gca 147

Leu Cys Ala Asn Ala Tyr Ser Arg Arg Thr Pro Ala Ser Gly Ala Ala	
30 35 40	
tta cag cag atg aac cgt gcc agt cag tca gtg aat tac cga cga cgt	195
Leu Gln Gln Met Asn Arg Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg	
45 50 55	
gag ctg tca tta atc agc ggc cgg aaa cag ggt gtc cag tct ctg ggt	243
Glu Leu Ser Leu Ile Ser Gly Arg Lys Gln Gly Val Gln Ser Leu Gly	
60 65 70	
tat aga ctt gca cgc ctc gat aac cgc gct ctt gca caa ttg ttg cac	291
Tyr Arg Leu Ala Arg Leu Asp Asn Arg Ala Leu Ala Gln Leu Leu His	
75 80 85 90	
agg gat ggc cag ccc gag gaa gtg gta cag cgc ggc aat gaa atc agc	339
Arg Asp Gly Gln Pro Glu Glu Val Val Gln Arg Gly Asn Glu Ile Ser	
95 100 105	
tat ttc gaa acg gga ctt gaa ccg acc acg ctt aga cgt gtg cgc gat	387
Tyr Phe Glu Thr Gly Leu Glu Pro Thr Thr Leu Arg Arg Val Arg Asp	
110 115 120	
tgt gtt gtt gcc gct ctg cca acc gtt atc tat acc gga ttc aaa cgt	435
Cys Val Val Ala Ala Leu Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg	
125 130 135	
gtt tct cct tac tac gaa ttt atc tcc gtc ggg cgc acg agg gtt gct	483
Val Ser Pro Tyr Tyr Glu Phe Ile Ser Val Gly Arg Thr Arg Val Ala	
140 145 150	
gat cgt ctt agc gaa gtc acg caa gtg gtt ccc cga gat gat aca cgc	531
Asp Arg Leu Ser Glu Val Thr Gln Val Val Pro Arg Asp Asp Thr Arg	
155 160 165 170	
tac gtc tac atc gtg tgg cgg gaa tcc gaa cga tcg aaa tta gag gcg	579
Tyr Val Tyr Ile Val Trp Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala	
175 180 185	
cgg ggg gat ctc cgt gat cgc gat ggt gaa acg ctg gaa aag ttt cgc	627
Arg Gly Asp Leu Arg Asp Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg	
190 195 200	
gtg att gct ttt aac gtc acg ctg gat atc agc agc agt atg gag ccg	675
Val Ile Ala Phe Asn Val Thr Leu Asp Ile Ser Ser Ser Met Glu Pro	
205 210 215	
ctg gcg aag gga gat ttg ccg ccg ttg ctt gct gtt cct gta ggt gaa	723
Leu Ala Lys Gly Asp Leu Pro Pro Leu Leu Ala Val Pro Val Gly Glu	
220 225 230	
caa gct aga ttc agc ttg acg cca acc tgg ttg cca cag ggt cgt agc	771
Gln Ala Arg Phe Ser Leu Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser	
235 240 245 250	
gat gtt tcc agt agt cga cgt ggg cta ccg cgg atg gac aaa gtg cct	819
Asp Val Ser Ser Ser Arg Arg Gly Leu Pro Arg Met Asp Lys Val Pro	

255										260										265										
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Ile Glu Ser Arg Leu Ser Thr Asp Gly Val Phe Ser Phe Ser Val Asn																														
270 275 280																														
gtt aac ggc gct acg cca tcg agg tgg gat cag atg ttg cgc acc gga	915																													
Val Asn Gly Ala Thr Pro Ser Arg Trp Asp Gln Met Leu Arg Thr Gly																														
285 290 295																														
cgc agg ccc gtc agt aga agc gta cgt gat gtc gcc gaa aac acc att	963																													
Arg Arg Pro Val Ser Arg Ser Val Arg Asp Val Ala Glu Asn Thr Ile																														
300 305 310																														
ggc ggt gaa ctg ccg ccg cgt agc tgc tcg cga ccc gat ccg ttg acc	1011																													
Gly Gly Glu Leu Pro Pro Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr																														
315 320 325 330																														
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Ala Asp Arg Arg Arg Cys Ala Ser Leu Ser Leu Pro Ser Leu Pro Ala																														
335 340 345																														
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Arg Gln Pro Ser Gln Thr Glu Lys Arg Ile Val Glu Asn Ile Lys Tyr																														
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35 40 45

Ala Ser Gln Ser Val Asn Tyr Arg Arg Arg Glu Leu Ser Leu Ile Ser
50 55 60

Gly Arg Lys Gln Gly Val Gln Ser Leu Gly Tyr Arg Leu Ala Arg Leu
65 70 75 80

Asp Asn Arg Ala Leu Ala Gln Leu Leu His Arg Asp Gly Gln Pro Glu
85 90 95

Glu Val Val Gln Arg Gly Asn Glu Ile Ser Tyr Phe Glu Thr Gly Leu
100 105 110

Glu Pro Thr Thr Leu Arg Arg Val Arg Asp Cys Val Val Ala Ala Leu
 115 120 125
 Pro Thr Val Ile Tyr Thr Gly Phe Lys Arg Val Ser Pro Tyr Tyr Glu
 130 135 140
 Phe Ile Ser Val Gly Arg Thr Arg Val Ala Asp Arg Leu Ser Glu Val
 145 150 155 160
 Thr Gln Val Val Pro Arg Asp Asp Thr Arg Tyr Val Tyr Ile Val Trp
 165 170 175
 Arg Glu Ser Glu Arg Ser Lys Leu Glu Ala Arg Gly Asp Leu Arg Asp
 180 185 190
 Arg Asp Gly Glu Thr Leu Glu Lys Phe Arg Val Ile Ala Phe Asn Val
 195 200 205
 Thr Leu Asp Ile Ser Ser Ser Met Glu Pro Leu Ala Lys Gly Asp Leu
 210 215 220
 Pro Pro Leu Leu Ala Val Pro Val Gly Glu Gln Ala Arg Phe Ser Leu
 225 230 235 240
 Thr Pro Thr Trp Leu Pro Gln Gly Arg Ser Asp Val Ser Ser Ser Arg
 245 250 255
 Arg Gly Leu Pro Arg Met Asp Lys Val Pro Ile Glu Ser Arg Leu Ser
 260 265 270
 Thr Asp Gly Val Phe Ser Phe Ser Val Asn Val Asn Gly Ala Thr Pro
 275 280 285
 Ser Arg Trp Asp Gln Met Leu Arg Thr Gly Arg Arg Pro Val Ser Arg
 290 295 300
 Ser Val Arg Asp Val Ala Glu Asn Thr Ile Gly Gly Glu Leu Pro Pro
 305 310 315 320
 Arg Ser Cys Ser Arg Pro Asp Pro Leu Thr Ala Asp Arg Arg Arg Cys
 325 330 335
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 Val Phe Asp Gly His Gly Gly Thr Asp Ala Ala His Phe
 130 135

gtt aga aag aac att ctg aga ttc att gta gag gac tcc tcc ttc cca 719
 Val Arg Lys Asn Ile Leu Arg Phe Ile Val Glu Asp Ser Ser Phe Pro
 140 145 150

cta tgc gta aag aaa gca att aag agt gct ttc tta aaa gct gat tat 767
 Leu Cys Val Lys Lys Ala Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr
 155 160 165 170

gaa ttt gca gat gat tct tct ctt gac atc tct tct ggg acc act gcg 815
 Glu Phe Ala Asp Asp Ser Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala
 175 180 185

ctt aca gct ttt att ttt gga cg gtaagagcat ttaaattcgt atttatgaac 868
 Leu Thr Ala Phe Ile Phe Gly Ar
 190

ttgggaagct atatatgtta tcacctgtat aatcatcaat acttatcagg ttgcctgtgt 928

gtataagata gagaataagg cttagtgtaa agacttatgt aacgggctgt tttaccatgt 988

ttctttgtag ttttgatgtg attttgaata gaattgctac tttctttctt tacag g 1044
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agg ttg ata att gca aat gct ggt gat tgc cga gca gta ctg ggg aga 1092
 Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu Gly Arg
 195 200 205 210

aga ggt agg gca att gag ttg tcc aaa gat cac aaa cca aac tgc aca 1140
 Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn Cys Thr
 215 220 225

gcc gag aaa gta aga ata gaa aag tta ggt gga gtt gtg tat gac ggt 1188
 Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr Asp Gly
 230 235 240

tac ctc aac ggg caa cta tca gtt gca cgt gcc att gga gac tgg cac 1236
 Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp Trp His
 245 250 255

atg aaa ggt ccc aaa ggc tct gct tgt ccg cta agc cca gag cca gag 1284
 Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu Pro Glu
 260 265 270

ttg caa gag aca gac ctg agt gaa gac gac gag ttc ttg ata atg gga 1332
 Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile Met Gly
 275 280 285 290

tgt gat ggt ctg tgg gat gtg atg agc agc cag tgc gct gtg aca ata 1380
 Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val Thr Ile
 295 300 305

gct agg aag gaa ctg atg att cat aat gat cca gag aga tgc tct aga 1428
 Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys Ser Arg
 310 315 320
 gag ctt gtg agg gag gcc ctt aaa cgg aat aca tgt gac aat ttg aca 1476
 Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn Leu Thr
 325 330 335
 gtg att gtt gtg tgc ttc tct ccg gat cct cca cag agg ata gag atc 1524
 Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile Glu Ile
 340 345 350
 cga atg cag tca cgg gtg agg cgg agc ata tct gcg gaa ggg tta aac 1572
 Arg Met Gln Ser Arg Val Arg Arg Ser Ile Ser Ala Glu Gly Leu Asn
 355 360 365 370
 cta ctc aaa ggc gtg ctc gat ggc tat ccg tga gcatgttatg ttgtacgtta 1625
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 35 40 45
 Thr Ser Ser Ala Thr Arg Leu Gln Leu Ala Ala Asn Ala Asp Val Asp
 50 55 60
 Val Cys Asn Leu Val Met Lys Ser Leu Asp Asp Lys Ser Glu Phe Leu
 65 70 75 80
 Pro Val Tyr Arg Ser Gly Ser Cys Ala Glu Gln Gly Ala Lys Gln Phe
 85 90 95
 Met Glu Asp Glu His Ile Cys Ile Asp Asp Leu Val Asn His Leu Gly
 100 105 110
 Ala Ala Ile Gln Cys Ser Ser Leu Gly Ala Phe Tyr Gly Val Phe Asp
 115 120 125
 Gly His Gly Gly Thr Asp Ala Ala His Phe Val Arg Lys Asn Ile Leu
 130 135 140

Arg Phe Ile Val Glu Asp Ser Ser Phe Pro Leu Cys Val Lys Lys Ala
 145 150 155 160
 Ile Lys Ser Ala Phe Leu Lys Ala Asp Tyr Glu Phe Ala Asp Asp Ser
 165 170 175
 Ser Leu Asp Ile Ser Ser Gly Thr Thr Ala Leu Thr Ala Phe Ile Phe
 180 185 190
 Gly Arg Arg Leu Ile Ile Ala Asn Ala Gly Asp Cys Arg Ala Val Leu
 195 200 205
 Gly Arg Arg Gly Arg Ala Ile Glu Leu Ser Lys Asp His Lys Pro Asn
 210 215 220
 Cys Thr Ala Glu Lys Val Arg Ile Glu Lys Leu Gly Gly Val Val Tyr
 225 230 235 240
 Asp Gly Tyr Leu Asn Gly Gln Leu Ser Val Ala Arg Ala Ile Gly Asp
 245 250 255
 Trp His Met Lys Gly Pro Lys Gly Ser Ala Cys Pro Leu Ser Pro Glu
 260 265 270
 Pro Glu Leu Gln Glu Thr Asp Leu Ser Glu Asp Asp Glu Phe Leu Ile
 275 280 285
 Met Gly Cys Asp Gly Leu Trp Asp Val Met Ser Ser Gln Cys Ala Val
 290 295 300
 Thr Ile Ala Arg Lys Glu Leu Met Ile His Asn Asp Pro Glu Arg Cys
 305 310 315 320
 Ser Arg Glu Leu Val Arg Glu Ala Leu Lys Arg Asn Thr Cys Asp Asn
 325 330 335
 Leu Thr Val Ile Val Val Cys Phe Ser Pro Asp Pro Pro Gln Arg Ile
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<400> 79

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Glu Val Pro Lys Val Ala Thr Glu Glu Ser Ser Ala Glu Val Thr Asp
                  15                20                25

cgt gga ttg ttc gat ttc ttg gga aag aag aaa gac gaa aca aaa cca      146
Arg Gly Leu Phe Asp Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro
                  30                35                40

gag gag act ccg atc gct tca gag ttt gag cag aag gtt cat att tca      194
Glu Glu Thr Pro Ile Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser
                  45                50                55

gag ccg gag cca gag gtt aaa cac gaa agt ctt ctt gaa aag ctt cac      242
Glu Pro Glu Pro Glu Val Lys His Glu Ser Leu Leu Glu Lys Leu His
                  60                65                70                75

cga agc gac agt tct tct agc tcc tca agt gag gaa gaa ggt tca gat      290
Arg Ser Asp Ser Ser Ser Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp
                  80                85                90

ggt gag aag agg aag aag aag aag gag aag aag aag cca act act gaa      338
Gly Glu Lys Arg Lys Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu
                  95                100                105

gtt gag gta aag gag gaa gag aag aaa ggg ttt atg gag aag ttg aaa      386
Val Glu Val Lys Glu Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys
                  110                115                120

gag aag ctt cct gga cac aag aaa cct gaa gac ggt tca gcc gtc gct      434
Glu Lys Leu Pro Gly His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala
                  125                130                135

gcg gca ccg gtg gtt gtt cct cct cct gtg gaa gaa gcg cat cca gtg      482
Ala Ala Pro Val Val Val Pro Pro Pro Val Glu Glu Ala His Pro Val
                  140                145                150                155

gag aag aaa ggg att ctt gag aag att aag gag aag ctt cca gga tac      530
Glu Lys Lys Gly Ile Leu Glu Lys Ile Lys Glu Lys Leu Pro Gly Tyr
                  160                165                170

cac cct aag acc acc gta gag gag gag aag aaa gat aaa gaa taa      575
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 Phe Leu Gly Lys Lys Lys Asp Glu Thr Lys Pro Glu Glu Thr Pro Ile
 35 40 45
 Ala Ser Glu Phe Glu Gln Lys Val His Ile Ser Glu Pro Glu Pro Glu
 50 55 60
 Val Lys His Glu Ser Leu Leu Glu Lys Leu His Arg Ser Asp Ser Ser
 65 70 75 80
 Ser Ser Ser Ser Ser Glu Glu Glu Gly Ser Asp Gly Glu Lys Arg Lys
 85 90 95
 Lys Lys Lys Glu Lys Lys Lys Pro Thr Thr Glu Val Glu Val Lys Glu
 100 105 110
 Glu Glu Lys Lys Gly Phe Met Glu Lys Leu Lys Glu Lys Leu Pro Gly
 115 120 125
 His Lys Lys Pro Glu Asp Gly Ser Ala Val Ala Ala Ala Pro Val Val
 130 135 140
 Val Pro Pro Pro Val Glu Glu Ala His Pro Val Glu Lys Lys Gly Ile
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 <213> Arabidopsis thaliana

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 <222> (20)..(1366)

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 Glu Val Ala Ala Arg Leu Ala Ala Glu Asp Leu His Asp Ile Asn Lys
 15 20 25
 tcc ggt ggt gct gat gtc aca atg tat aag gtg acg gag aga aca act 148

Ser	Gly	Gly	Ala	Asp	Val	Thr	Met	Tyr	Lys	Val	Thr	Glu	Arg	Thr	Thr		
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gaa	cat	cca	ccg	gag	caa	gat	agg	ccc	ggt	gtg	ata	ggt	tca	gtg	ttc	196	
Glu	His	Pro	Pro	Glu	Gln	Asp	Arg	Pro	Gly	Val	Ile	Gly	Ser	Val	Phe		
	45					50				55							
agg	gct	gtc	caa	gga	acg	tat	gag	cat	gcg	aga	gac	gct	gta	gtt	gga	244	
Arg	Ala	Val	Gln	Gly	Thr	Tyr	Glu	His	Ala	Arg	Asp	Ala	Val	Val	Gly		
	60				65				70					75			
aaa	acc	cac	gaa	gcg	gct	gag	tct	acc	aaa	gaa	gga	gct	cag	ata	gct	292	
Lys	Thr	His	Glu	Ala	Ala	Glu	Ser	Thr	Lys	Glu	Gly	Ala	Gln	Ile	Ala		
			80						85					90			
tca	gag	aaa	gcg	gtt	gga	gca	aag	gac	gca	acc	gtc	gag	aaa	gct	aag	340	
Ser	Glu	Lys	Ala	Val	Gly	Ala	Lys	Asp	Ala	Thr	Val	Glu	Lys	Ala	Lys		
		95						100					105				
gaa	acc	gct	gat	tat	act	gcg	gag	aag	gtg	ggt	gag	tat	aaa	gac	tat	388	
Glu	Thr	Ala	Asp	Tyr	Thr	Ala	Glu	Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr		
	110					115						120					
acg	gtt	gat	aaa	gct	aaa	gag	gct	aag	gac	aca	act	gca	gag	aag	gcg	436	
Thr	Val	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Thr	Thr	Ala	Glu	Lys	Ala		
	125					130					135						
aag	gag	act	gct	aat	tat	act	gcg	gat	aag	gcg	gtg	gaa	gca	aag	gat	484	
Lys	Glu	Thr	Ala	Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Val	Glu	Ala	Lys	Asp		
	140				145				150						155		
aag	acg	gcg	gag	aag	att	ggt	gag	tac	aaa	gac	tat	gcg	gtg	gat	aag	532	
Lys	Thr	Ala	Glu	Lys	Ile	Gly	Glu	Tyr	Lys	Asp	Tyr	Ala	Val	Asp	Lys		
			160						165					170			
gca	gta	gaa	gct	aaa	gat	aag	aca	gcg	gag	aag	gcg	aag	gag	act	tcg	580	
Ala	Val	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu	Lys	Ala	Lys	Glu	Thr	Ser		
		175						180						185			
aat	tat	acg	gcg	gat	aag	gct	aaa	gag	gct	aag	gac	aag	acg	gct	gag	628	
Asn	Tyr	Thr	Ala	Asp	Lys	Ala	Lys	Glu	Ala	Lys	Asp	Lys	Thr	Ala	Glu		
	190						195					200					
aag	gtt	ggt	gag	tat	aag	gat	tac	acg	gtg	gac	aag	gcc	gtg	gaa	gct	676	
Lys	Val	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Asp	Lys	Ala	Val	Glu	Ala		
	205				210						215						
agg	gat	tac	aca	gcg	gag	aag	gct	att	gaa	gca	aag	gat	aag	aca	gct	724	
Arg	Asp	Tyr	Thr	Ala	Glu	Lys	Ala	Ile	Glu	Ala	Lys	Asp	Lys	Thr	Ala		
	220				225					230					235		
gag	aag	act	gga	gag	tat	aag	gac	tat	acg	gtg	gag	aag	gcg	acg	gag	772	
Glu	Lys	Thr	Gly	Glu	Tyr	Lys	Asp	Tyr	Thr	Val	Glu	Lys	Ala	Thr	Glu		
			240					245						250			
ggg	aaa	gat	gtt	acg	gtg	agt	aag	cta	gga	gag	ctg	aag	gat	agt	gcc	820	
Gly	Lys	Asp	Val	Thr	Val	Ser	Lys	Leu	Gly	Glu	Leu	Lys	Asp	Ser	Ala		

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Val Glu Thr Ala Lys Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu				
	270	275	280	
gag gcc aaa gga aaa gct gtg gag acc aaa gat act gcc aag gaa aac				916
Glu Ala Lys Gly Lys Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn				
	285	290	295	
atg gag aaa gct gga gaa gta aca aga caa aag atg gag gaa atg aga				964
Met Glu Lys Ala Gly Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg				
	300	305	310	315
ttg gaa ggt aaa gag ctc aaa gaa gaa gct gga gca aaa gcc caa gag				1012
Leu Glu Gly Lys Glu Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu				
	320	325	330	
gca tct caa aag act agg gag agt act gag tcg gga gct caa aaa gcc				1060
Ala Ser Gln Lys Thr Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala				
	335	340	345	
gaa gag acc aaa gat tct cct gcc gtg agg gga aat gaa gcg aaa ggg				1108
Glu Glu Thr Lys Asp Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly				
	350	355	360	
act att ttt ggt gca tta ggg aat gta acg gaa gca ata aag agc aaa				1156
Thr Ile Phe Gly Ala Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys				
	365	370	375	
ctg aca atg cca tca gac att gtg gag gaa aca cgc gcg gca cgt gag				1204
Leu Thr Met Pro Ser Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu				
	380	385	390	395
cat gga ggg acg ggt agg act gtg gtt gaa gtc aag gtc gag gat tca				1252
His Gly Gly Thr Gly Arg Thr Val Val Glu Val Lys Val Glu Asp Ser				
	400	405	410	
aag ccg ggt aag gtg gcg act tca ctg aag gcg tcg gat caa atg acc				1300
Lys Pro Gly Lys Val Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr				
	415	420	425	
ggt caa aca ttc aac gac gtt gga cgg atg gat gat gat gct cgg aaa				1348
Gly Gln Thr Phe Asn Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys				
	430	435	440	
gat aag gga aag ctg tga gaatactaga				1376
Asp Lys Gly Lys Leu				
	445			

<210> 82

<211> 448

<212> PRT

<213> Arabidopsis thaliana

<400> 82

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 20 25 30
 Val Thr Met Tyr Lys Val Thr Glu Arg Thr Thr Glu His Pro Pro Glu
 35 40 45
 Gln Asp Arg Pro Gly Val Ile Gly Ser Val Phe Arg Ala Val Gln Gly
 50 55 60
 Thr Tyr Glu His Ala Arg Asp Ala Val Val Gly Lys Thr His Glu Ala
 65 70 75 80
 Ala Glu Ser Thr Lys Glu Gly Ala Gln Ile Ala Ser Glu Lys Ala Val
 85 90 95
 Gly Ala Lys Asp Ala Thr Val Glu Lys Ala Lys Glu Thr Ala Asp Tyr
 100 105 110
 Thr Ala Glu Lys Val Gly Glu Tyr Lys Asp Tyr Thr Val Asp Lys Ala
 115 120 125
 Lys Glu Ala Lys Asp Thr Thr Ala Glu Lys Ala Lys Glu Thr Ala Asn
 130 135 140
 Tyr Thr Ala Asp Lys Ala Val Glu Ala Lys Asp Lys Thr Ala Glu Lys
 145 150 155 160
 Ile Gly Glu Tyr Lys Asp Tyr Ala Val Asp Lys Ala Val Glu Ala Lys
 165 170 175
 Asp Lys Thr Ala Glu Lys Ala Lys Glu Thr Ser Asn Tyr Thr Ala Asp
 180 185 190
 Lys Ala Lys Glu Ala Lys Asp Lys Thr Ala Glu Lys Val Gly Glu Tyr
 195 200 205
 Lys Asp Tyr Thr Val Asp Lys Ala Val Glu Ala Arg Asp Tyr Thr Ala
 210 215 220
 Glu Lys Ala Ile Glu Ala Lys Asp Lys Thr Ala Glu Lys Thr Gly Glu
 225 230 235 240
 Tyr Lys Asp Tyr Thr Val Glu Lys Ala Thr Glu Gly Lys Asp Val Thr
 245 250 255
 Val Ser Lys Leu Gly Glu Leu Lys Asp Ser Ala Val Glu Thr Ala Lys
 260 265 270
 Arg Ala Met Gly Phe Leu Ser Gly Lys Thr Glu Glu Ala Lys Gly Lys
 275 280 285
 Ala Val Glu Thr Lys Asp Thr Ala Lys Glu Asn Met Glu Lys Ala Gly
 290 295 300

Glu Val Thr Arg Gln Lys Met Glu Glu Met Arg Leu Glu Gly Lys Glu
 305 310 315 320
 Leu Lys Glu Glu Ala Gly Ala Lys Ala Gln Glu Ala Ser Gln Lys Thr
 325 330 335
 Arg Glu Ser Thr Glu Ser Gly Ala Gln Lys Ala Glu Glu Thr Lys Asp
 340 345 350
 Ser Pro Ala Val Arg Gly Asn Glu Ala Lys Gly Thr Ile Phe Gly Ala
 355 360 365
 Leu Gly Asn Val Thr Glu Ala Ile Lys Ser Lys Leu Thr Met Pro Ser
 370 375 380
 Asp Ile Val Glu Glu Thr Arg Ala Ala Arg Glu His Gly Gly Thr Gly
 385 390 395 400
 Arg Thr Val Val Glu Val Lys Val Glu Asp Ser Lys Pro Gly Lys Val
 405 410 415
 Ala Thr Ser Leu Lys Ala Ser Asp Gln Met Thr Gly Gln Thr Phe Asn
 420 425 430
 Asp Val Gly Arg Met Asp Asp Asp Ala Arg Lys Asp Lys Gly Lys Leu
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<210> 83
 <211> 561
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<220>
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 <222> (18) .. (548)

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 1 5 10
 atc gta gta gca tta ttc ttc gat tta act caa gcc tat cgt cac act 98
 Ile Val Val Ala Leu Phe Phe Asp Leu Thr Gln Ala Tyr Arg His Thr
 15 20 25
 ccc gct caa ccg cca aaa gca aac gca aac ggt gat gtc aaa ccg caa 146
 Pro Ala Gln Pro Pro Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln
 30 35 40
 gaa acg ctc gtg gtt cac aac aag gcc cga gcc atg gtc gga gtc gga 194
 Glu Thr Leu Val Val His Asn Lys Ala Arg Ala Met Val Gly Val Gly
 45 50 55
 cca atg gtg tgg aac gaa act ctt gcg acc tat gca cag agc tac gca 242
 Pro Met Val Trp Asn Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala

60	65	70	75	
cat gaa cga gcc aga gac tgt gcc atg aag cat tcc ttg gga cca ttc				290
His Glu Arg Ala Arg Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe	80	85	90	
ggc gag aat cta gcc gcg ggt tgg gga acg atg agc ggt ccg gta gca				338
Gly Glu Asn Leu Ala Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala	95	100	105	
act gag tat tgg atg acg gag aag gaa aat tac gat tat gat agt aac				386
Thr Glu Tyr Trp Met Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn	110	115	120	
acg tgt ggt ggt gat ggt gtg tgt gga cac tac act cag atc gtg tgg				434
Thr Cys Gly Gly Asp Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp	125	130	135	
cgt gac tcg gtt cga ctt ggt tgt gcc tcc gtg aga tgt aag aat gat				482
Arg Asp Ser Val Arg Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp	140	145	150	155
gag tat att tgg gtg att tgt agc tat gat cct ccg ggg aat tac atc				530
Glu Tyr Ile Trp Val Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile	160	165	170	
ggg caa cgt cca tat tag tgattggatt tta				561
Gly Gln Arg Pro Tyr	175			

<210> 84

<211> 176

<212> PRT

<213> Arabidopsis thaliana

<400> 84

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20 25 30

Lys Ala Asn Ala Asn Gly Asp Val Lys Pro Gln Glu Thr Leu Val Val
35 40 45

His Asn Lys Ala Arg Ala Met Val Gly Val Gly Pro Met Val Trp Asn
50 55 60

Glu Thr Leu Ala Thr Tyr Ala Gln Ser Tyr Ala His Glu Arg Ala Arg
65 70 75 80

Asp Cys Ala Met Lys His Ser Leu Gly Pro Phe Gly Glu Asn Leu Ala
85 90 95

Ala Gly Trp Gly Thr Met Ser Gly Pro Val Ala Thr Glu Tyr Trp Met
100 105 110

Thr Glu Lys Glu Asn Tyr Asp Tyr Asp Ser Asn Thr Cys Gly Gly Asp
 115 120 125
 Gly Val Cys Gly His Tyr Thr Gln Ile Val Trp Arg Asp Ser Val Arg
 130 135 140
 Leu Gly Cys Ala Ser Val Arg Cys Lys Asn Asp Glu Tyr Ile Trp Val
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 Ile Cys Ser Tyr Asp Pro Pro Gly Asn Tyr Ile Gly Gln Arg Pro Tyr
 165 170 175

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 <211> 988
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 <213> Arabidopsis thaliana

<220>
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 <222> (12) .. (977)

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 Leu Val Leu Leu Phe Ala Gln Ala Asn Ser Gln Gly Leu Lys Val Gly
 15 20 25
 ttc tac agc aaa aca tgc cca caa ctc gag ggt ata gtt aaa aag gtc 146
 Phe Tyr Ser Lys Thr Cys Pro Gln Leu Glu Gly Ile Val Lys Lys Val
 30 35 40 45
 gtg ttc gat gcg atg aac aaa gca cca aca ctt ggt gct cct ttg ctt 194
 Val Phe Asp Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu
 50 55 60
 aga atg ttc ttc cac gac tgc ttc gtt cgg gga tgt gac gga tca gtt 242
 Arg Met Phe Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val
 65 70 75
 ttg tta gat aaa cca aac aat caa ggt gag aag agt gca gtt cct aac 290
 Leu Leu Asp Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn
 80 85 90
 cta agt ctt cga ggg ttt ggc atc ata gac gat tcc aag gcg gct cta 338
 Leu Ser Leu Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu
 95 100 105
 gaa aaa gtg tgt ccg gga att gtt tct tgc tct gat atc ttg gca ctt 386
 Glu Lys Val Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu
 110 115 120 125

gtc gct aga gac gca atg gtt gca ctt gaa gga cca tca tgg gaa gtt	434
Val Ala Arg Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val	
130 135 140	
gaa acg gga aga aga gac ggt agg gtt tct aac atc aac gaa gtc aac	482
Glu Thr Gly Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn	
145 150 155	
ttg cca tca cct ttt gat aac atc acc aag ctt atc agc gat ttt cgc	530
Leu Pro Ser Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg	
160 165 170	
tca aag ggc ctc aac gag aag gat cta gtc att ctc tcg ggt ggt cac	578
Ser Lys Gly Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His	
175 180 185	
aca att gga atg gga cat tgt cct tta ttg aca aac cgg ctt tac aac	626
Thr Ile Gly Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn	
190 195 200 205	
ttc acc gga aaa gga gac agc gac cca agt ttg gac tcg gag tac gcc	674
Phe Thr Gly Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala	
210 215 220	
gct aag ctc agg aag aaa tgc aag ccc acc gat acg acg acg gct cta	722
Ala Lys Leu Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu	
225 230 235	
gag atg gat ccg ggg agt ttc aaa aca ttt gac ttg agc tac ttc acg	770
Glu Met Asp Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr	
240 245 250	
cta gtg gct aag aga aga gga ctt ttc cag tcg gat gct gct cta ctc	818
Leu Val Ala Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu	
255 260 265	
gac aac tcc aag act agg gct tat gtc ttg caa cag ata aga act cat	866
Asp Asn Ser Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His	
270 275 280 285	
ggg tca atg ttc ttt aac gac ttt ggt gtc tct atg gtg aaa atg ggt	914
Gly Ser Met Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly	
290 295 300	
cgg act gga gtt ctt acg ggt aag gcc ggg gag atc cgt aag acg tgt	962
Arg Thr Gly Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys	
305 310 315	
cgg tct gct aat taa gagatataga aa	989
Arg Ser Ala Asn	
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<210> 86

<211> 321

<212> PRT

<213> Arabidopsis thaliana

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 35 40 45
 Ala Met Asn Lys Ala Pro Thr Leu Gly Ala Pro Leu Leu Arg Met Phe
 50 55 60
 Phe His Asp Cys Phe Val Arg Gly Cys Asp Gly Ser Val Leu Leu Asp
 65 70 75 80
 Lys Pro Asn Asn Gln Gly Glu Lys Ser Ala Val Pro Asn Leu Ser Leu
 85 90 95
 Arg Gly Phe Gly Ile Ile Asp Asp Ser Lys Ala Ala Leu Glu Lys Val
 100 105 110
 Cys Pro Gly Ile Val Ser Cys Ser Asp Ile Leu Ala Leu Val Ala Arg
 115 120 125
 Asp Ala Met Val Ala Leu Glu Gly Pro Ser Trp Glu Val Glu Thr Gly
 130 135 140
 Arg Arg Asp Gly Arg Val Ser Asn Ile Asn Glu Val Asn Leu Pro Ser
 145 150 155 160
 Pro Phe Asp Asn Ile Thr Lys Leu Ile Ser Asp Phe Arg Ser Lys Gly
 165 170 175
 Leu Asn Glu Lys Asp Leu Val Ile Leu Ser Gly Gly His Thr Ile Gly
 180 185 190
 Met Gly His Cys Pro Leu Leu Thr Asn Arg Leu Tyr Asn Phe Thr Gly
 195 200 205
 Lys Gly Asp Ser Asp Pro Ser Leu Asp Ser Glu Tyr Ala Ala Lys Leu
 210 215 220
 Arg Lys Lys Cys Lys Pro Thr Asp Thr Thr Thr Ala Leu Glu Met Asp
 225 230 235 240
 Pro Gly Ser Phe Lys Thr Phe Asp Leu Ser Tyr Phe Thr Leu Val Ala
 245 250 255
 Lys Arg Arg Gly Leu Phe Gln Ser Asp Ala Ala Leu Leu Asp Asn Ser
 260 265 270
 Lys Thr Arg Ala Tyr Val Leu Gln Gln Ile Arg Thr His Gly Ser Met
 275 280 285
 Phe Phe Asn Asp Phe Gly Val Ser Met Val Lys Met Gly Arg Thr Gly

125

290 295 300

Val Leu Thr Gly Lys Ala Gly Glu Ile Arg Lys Thr Cys Arg Ser Ala
 305 310 315 320

Asn

<210> 87
 <211> 650
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (8)..(634)

<400> 87

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	1				5					10						
tcg	ttc	tcc	tcc	caa	gtt	tct	caa	aga	cct	aac	acc	att	tcc	ttc	ccc	97
Ser	Phe	Ser	Ser	Gln	Val	Ser	Gln	Arg	Pro	Asn	Thr	Ile	Ser	Phe	Pro	
15				20					25					30		
cgc	gcg	aat	tca	gta	ttc	gca	tta	ccg	gcg	aaa	tcc	gca	cgc	cgc	gct	145
Arg	Ala	Asn	Ser	Val	Phe	Ala	Leu	Pro	Ala	Lys	Ser	Ala	Arg	Arg	Ala	
			35					40					45			
tct	cta	tct	atc	acc	gcc	acg	gta	tct	gct	cca	ccg	gag	gag	gag	gag	193
Ser	Leu	Ser	Ile	Thr	Ala	Thr	Val	Ser	Ala	Pro	Pro	Glu	Glu	Glu	Glu	
			50				55						60			
ata	gtt	gaa	ctg	aag	aaa	tac	gtc	aaa	tcg	agg	ctt	ccc	gga	gga	ttt	241
Ile	Val	Glu	Leu	Lys	Lys	Tyr	Val	Lys	Ser	Arg	Leu	Pro	Gly	Gly	Phe	
	65					70						75				
gct	gct	cag	aag	att	att	ggc	act	gga	cga	cgt	aag	tgc	gca	atc	gct	289
Ala	Ala	Gln	Lys	Ile	Ile	Gly	Thr	Gly	Arg	Arg	Lys	Cys	Ala	Ile	Ala	
	80					85					90					
aga	gtt	gtt	ctt	cag	gaa	ggt	act	ggg	aag	gtt	atc	atc	aac	tat	cgt	337
Arg	Val	Val	Leu	Gln	Glu	Gly	Thr	Gly	Lys	Val	Ile	Ile	Asn	Tyr	Arg	
95				100						105				110		
gat	gcc	aag	gag	tac	ctt	cag	gga	aat	cca	ttg	tgg	ctt	cag	tat	gtt	385
Asp	Ala	Lys	Glu	Tyr	Leu	Gln	Gly	Asn	Pro	Leu	Trp	Leu	Gln	Tyr	Val	
			115						120				125			
aaa	gta	cca	ttg	gtg	act	tta	gga	tat	gag	aat	agc	tac	gac	ata	ttt	433
Lys	Val	Pro	Leu	Val	Thr	Leu	Gly	Tyr	Glu	Asn	Ser	Tyr	Asp	Ile	Phe	
		130					135					140				
gtg	aaa	gcc	cat	gga	ggc	ggt	ctc	tca	ggt	caa	gct	caa	gca	att	acc	481
Val	Lys	Ala	His	Gly	Gly	Gly	Leu	Ser	Gly	Gln	Ala	Gln	Ala	Ile	Thr	

145	150	155	
ttg gga gtc gca cgt gca ctc ctg aag gta agt gca gac cac aga tcg			529
Leu Gly Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser			
160	165	170	
cct ttg aag aag gaa ggt ttg ctc act aga gat gcg aga gtg gtt gaa			577
Pro Leu Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu			
175	180	185	190
aga aag aag gcc ggg ctc aag aag gcg cgt aaa gcc cca caa ttc tcc			625
Arg Lys Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser			
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Lys Arg			
<210> 88			
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<213> Arabidopsis thaliana			
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Asn Ser Val Phe Ala Leu Pro Ala Lys Ser Ala Arg Arg Ala Ser Leu			
35	40	45	
Ser Ile Thr Ala Thr Val Ser Ala Pro Pro Glu Glu Glu Glu Ile Val			
50	55	60	
Glu Leu Lys Lys Tyr Val Lys Ser Arg Leu Pro Gly Gly Phe Ala Ala			
65	70	75	80
Gln Lys Ile Ile Gly Thr Gly Arg Arg Lys Cys Ala Ile Ala Arg Val			
85	90	95	
Val Leu Gln Glu Gly Thr Gly Lys Val Ile Ile Asn Tyr Arg Asp Ala			
100	105	110	
Lys Glu Tyr Leu Gln Gly Asn Pro Leu Trp Leu Gln Tyr Val Lys Val			
115	120	125	
Pro Leu Val Thr Leu Gly Tyr Glu Asn Ser Tyr Asp Ile Phe Val Lys			
130	135	140	
Ala His Gly Gly Gly Leu Ser Gly Gln Ala Gln Ala Ile Thr Leu Gly			
145	150	155	160
Val Ala Arg Ala Leu Leu Lys Val Ser Ala Asp His Arg Ser Pro Leu			
165	170	175	

Lys Lys Glu Gly Leu Leu Thr Arg Asp Ala Arg Val Val Glu Arg Lys
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Lys Ala Gly Leu Lys Lys Ala Arg Lys Ala Pro Gln Phe Ser Lys Arg
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<210> 89

<211> 1223

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (16)..(1215)

<400> 89

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gag atg gct cgg act cag aag aat aaa gct aca gag tat cat ctt ggt 99
Glu Met Ala Arg Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly
      15              20              25

cag ctc aag gca aag att gca aaa ctc agg aca caa ctg ttg gag cct 147
Gln Leu Lys Ala Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro
      30              35              40

cca aaa ggt gct agt gga ggc ggg gaa ggt ttt gaa gtt acc aag tat 195
Pro Lys Gly Ala Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr
      45              50              55              60

ggt cat gga cgt gtt gca ctt ata gga ttt cct agt gtc gga aag tcc 243
Gly His Gly Arg Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser
      65              70              75

acg ctt ttg act atg tta act gga aca cat tct gaa gca gcc tca tat 291
Thr Leu Leu Thr Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr
      80              85              90

gaa ttt aca aca ctt aca tgc atc cct ggt gta att cac tac aac gac 339
Glu Phe Thr Thr Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp
      95              100              105

aca aag att cag ctt ctc gat ctt cct ggg att att gaa ggt gct tcg 387
Thr Lys Ile Gln Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser
      110              115              120

gaa gga aag ggg cga gga agg cag gtt att gct gtt gca aag tct tcc 435
Glu Gly Lys Gly Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser
      125              130              135              140

gac ctt gta ttg atg gtt ctt gat gcc tca aaa agc gaa ggc cac agg 483
Asp Leu Val Leu Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg
      145              150              155

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Gln Ile Leu Thr Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys	
160 165 170	
act cct ccg cag ata tac ttt aaa aag aaa aag act ggt gga atc tct	579
Thr Pro Pro Gln Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser	
175 180 185	
ttc aac act aca gca ccc ttg act cac att gat gag aag ctc tgt tat	627
Phe Asn Thr Thr Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr	
190 195 200	
caa atc ctg cat gaa tac aag att cac aat gct gag gtg cta ttt cgt	675
Gln Ile Leu His Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg	
205 210 215 220	
gag aat gcc aca gtg gat gac ttt att gat gtc att gaa ggc aac cgc	723
Glu Asn Ala Thr Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg	
225 230 235	
aag tat att aag tgt gtt tat gtc tac atc aaa ata gat gtt gtt gga	771
Lys Tyr Ile Lys Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly	
240 245 250	
att gat gat gtg gat aga cta tcc cgg cag cca aat tcc att gtt att	819
Ile Asp Asp Val Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile	
255 260 265	
agc tgc aat ctt aag ctt aac tta gac aga cta ctt gct agg atg tgg	867
Ser Cys Asn Leu Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp	
270 275 280	
gac gaa atg ggc ctt gtg aga gtt tac tcg aag ccg caa ggc cag caa	915
Asp Glu Met Gly Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln	
285 290 295 300	
cca gat ttc gat gag cct ttt gtc ctc tca tct gat cga ggt ggc tgc	963
Pro Asp Phe Asp Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys	
305 310 315	
aca gtg gaa gac ttc tgt aac cac gtc cac agg act ctg gtg aag gat	1011
Thr Val Glu Asp Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp	
320 325 330	
atg aag tat gca ctc gtt tgg ggc aca agc aca agg cac aat cca cag	1059
Met Lys Tyr Ala Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln	
335 340 345	
aat tgt ggt ctt tct caa cat ctt gaa gac gaa gat gtt gtt cag atc	1107
Asn Cys Gly Leu Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile	
350 355 360	
gtc aag aaa aag gag aga gac gaa gga gga aga ggc cgg ttc aag tca	1155
Val Lys Lys Lys Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser	
365 370 375 380	

cac tca aac gcc cct gct aga att gca gac aga gag aaa aaa gct cct 1203
 His Ser Asn Ala Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro
 385 390 395

ctt aag caa taa gcttttag 1223
 Leu Lys Gln
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<210> 90

<211> 399

<212> PRT

<213> Arabidopsis thaliana

<400> 90

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Thr Gln Lys Asn Lys Ala Thr Glu Tyr His Leu Gly Gln Leu Lys Ala
 20 25 30

Lys Ile Ala Lys Leu Arg Thr Gln Leu Leu Glu Pro Pro Lys Gly Ala
 35 40 45

Ser Gly Gly Gly Glu Gly Phe Glu Val Thr Lys Tyr Gly His Gly Arg
 50 55 60

Val Ala Leu Ile Gly Phe Pro Ser Val Gly Lys Ser Thr Leu Leu Thr
 65 70 75 80

Met Leu Thr Gly Thr His Ser Glu Ala Ala Ser Tyr Glu Phe Thr Thr
 85 90 95

Leu Thr Cys Ile Pro Gly Val Ile His Tyr Asn Asp Thr Lys Ile Gln
 100 105 110

Leu Leu Asp Leu Pro Gly Ile Ile Glu Gly Ala Ser Glu Gly Lys Gly
 115 120 125

Arg Gly Arg Gln Val Ile Ala Val Ala Lys Ser Ser Asp Leu Val Leu
 130 135 140

Met Val Leu Asp Ala Ser Lys Ser Glu Gly His Arg Gln Ile Leu Thr
 145 150 155 160

Lys Glu Leu Glu Ala Val Gly Leu Arg Leu Asn Lys Thr Pro Pro Gln
 165 170 175

Ile Tyr Phe Lys Lys Lys Lys Thr Gly Gly Ile Ser Phe Asn Thr Thr
 180 185 190

Ala Pro Leu Thr His Ile Asp Glu Lys Leu Cys Tyr Gln Ile Leu His
 195 200 205

Glu Tyr Lys Ile His Asn Ala Glu Val Leu Phe Arg Glu Asn Ala Thr
 210 215 220

Val Asp Asp Phe Ile Asp Val Ile Glu Gly Asn Arg Lys Tyr Ile Lys
225 230 235 240

Cys Val Tyr Val Tyr Ile Lys Ile Asp Val Val Gly Ile Asp Asp Val
245 250 255

Asp Arg Leu Ser Arg Gln Pro Asn Ser Ile Val Ile Ser Cys Asn Leu
260 265 270

Lys Leu Asn Leu Asp Arg Leu Leu Ala Arg Met Trp Asp Glu Met Gly
275 280 285

Leu Val Arg Val Tyr Ser Lys Pro Gln Gly Gln Gln Pro Asp Phe Asp
290 295 300

Glu Pro Phe Val Leu Ser Ser Asp Arg Gly Gly Cys Thr Val Glu Asp
305 310 315 320

Phe Cys Asn His Val His Arg Thr Leu Val Lys Asp Met Lys Tyr Ala
325 330 335

Leu Val Trp Gly Thr Ser Thr Arg His Asn Pro Gln Asn Cys Gly Leu
340 345 350

Ser Gln His Leu Glu Asp Glu Asp Val Val Gln Ile Val Lys Lys Lys
355 360 365

Glu Arg Asp Glu Gly Gly Arg Gly Arg Phe Lys Ser His Ser Asn Ala
370 375 380

Pro Ala Arg Ile Ala Asp Arg Glu Lys Lys Ala Pro Leu Lys Gln
385 390 395

<210> 91

<211> 536

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (12)..(524)

<400> 91

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Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe
1 5 10

gtc tac ggc agt ttc caa gaa cca gcc gtt gtt aat tta att ctc gaa 98
Val Tyr Gly Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu
15 20 25

tgt gct ccg gtc atg gtt tcc gct caa ctc cac ggc tat cac ttg tat 146
Cys Ala Pro Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr
30 35 40 45

aga ctt aaa ggt cgt ttg cat cca tgt att tct cct tcc gac aat gga 194
 Arg Leu Lys Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly
 50 55 60

tta atc aat ggc aag ata cta act gga tta aca gat tct cag tta gag 242
 Leu Ile Asn Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu
 65 70 75

agt tta gat atg att gaa gga act gaa tat gtg agg aag act gtt gaa 290
 Ser Leu Asp Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu
 80 85 90

gtt gtt ttg act gat act ttg gag aag aag caa gtt gaa aca att gta 338
 Val Val Leu Thr Asp Thr Leu Glu Lys Lys Gln Val Glu Thr Ile Val
 95 100 105

tgg gca aac aag gat gat cct aat atg tat gga gaa tgg gat ttc gag 386
 Trp Ala Asn Lys Asp Asp Pro Asn Met Tyr Gly Glu Trp Asp Phe Glu
 110 115 120 125

gaa tgg aag agg ctt cat atg gag aaa ttt ata gag gcg gcg acg aaa 434
 Glu Trp Lys Arg Leu His Met Glu Lys Phe Ile Glu Ala Ala Thr Lys
 130 135 140

ttc atg gag tgg aag aag aat ccg aat ggg aga agt agg gaa gag ttt 482
 Phe Met Glu Trp Lys Lys Asn Pro Asn Gly Arg Ser Arg Glu Glu Phe
 145 150 155

gag aag ttt gta caa gat gat tct tct ccg gct tcg gct tga 524
 Glu Lys Phe Val Gln Asp Asp Ser Ser Pro Ala Ser Ala
 160 165 170

agaagttggt ta 536

<210> 92

<211> 170

<212> PRT

<213> Arabidopsis thaliana

<400> 92

Met Thr Ser Ser Asp Gln Ser Pro Ser His Asp Val Phe Val Tyr Gly
 1 5 10 15

Ser Phe Gln Glu Pro Ala Val Val Asn Leu Ile Leu Glu Cys Ala Pro
 20 25 30

Val Met Val Ser Ala Gln Leu His Gly Tyr His Leu Tyr Arg Leu Lys
 35 40 45

Gly Arg Leu His Pro Cys Ile Ser Pro Ser Asp Asn Gly Leu Ile Asn
 50 55 60

Gly Lys Ile Leu Thr Gly Leu Thr Asp Ser Gln Leu Glu Ser Leu Asp
 65 70 75 80

Met Ile Glu Gly Thr Glu Tyr Val Arg Lys Thr Val Glu Val Val Leu

<210> 94

<211> 45
 <212> PRT
 <213> Arabidopsis thaliana

<400> 94
 Met Ala Gly Ser Asn Cys Gly Cys Gly Ser Ser Cys Lys Cys Gly Asp
 1 5 10 15
 Ser Cys Ser Cys Glu Lys Asn Tyr Asn Lys Glu Cys Asp Asn Cys Ser
 20 25 30
 Cys Gly Ser Asn Cys Ser Cys Gly Ser Ser Cys Asn Cys
 35 40 45

<210> 95
 <211> 880
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (14)..(868)

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 Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile
 1 5 10
 cgc ctc aga tct ctc gct ctt tcg tct tct ttt tct tct ttc cga ttt 97
 Arg Leu Arg Ser Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe
 15 20 25
 gcc cat cgt cct ctg tca tcg att tca ccg aga aag tta ccg aat ttt 145
 Ala His Arg Pro Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe
 30 35 40
 cgt gct ttc tct ggt acc gct atg aca gat act aaa gat gct ggt atg 193
 Arg Ala Phe Ser Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met
 45 50 55 60
 gat gct gtt cag aga cgt ctc atg ttt gag gat gaa tgc att ctt gtt 241
 Asp Ala Val Gln Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val
 65 70 75
 gat gaa act gat cgt gtt gtg ggg cat gac agc aag tat aat tgt cat 289
 Asp Glu Thr Asp Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His
 80 85 90
 ctg atg gaa aat att gaa gcc aag aat ttg ctg cac agg gct ttt agt 337
 Leu Met Glu Asn Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser
 95 100 105
 gta ttt tta ttc aac tcg aag tat gag ttg ctt ctc cag caa agg tca 385
 Val Phe Leu Phe Asn Ser Lys Tyr Glu Leu Leu Gln Gln Arg Ser
 110 115 120

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aac aca aag gtt acg ttc cct cta gtg tgg act aac act tgt tgc agc 433
Asn Thr Lys Val Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser
125 130 135 140

cat cct ctt tac cgt gaa tca gag ctt atc cag gac aat gca cta ggt 481
His Pro Leu Tyr Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly
145 150 155

gtg agg aat gct gca caa aga aag ctt ctc gat gag ctt ggt att gta 529
Val Arg Asn Ala Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val
160 165 170

gct gaa gat gta cca gtc gat gag ttc act ccc ttg gga cgt atg ctg 577
Ala Glu Asp Val Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu
175 180 185

tac aag gct cct tct gat ggc aaa tgg gga gag cat gaa ctt gat tac 625
Tyr Lys Ala Pro Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr
190 195 200

ttg ctc ttc atc gtg cga gac gtg aag gtt caa cca aac cca gat gaa 673
Leu Leu Phe Ile Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu
205 210 215 220

gta gct gag atc aag tat gtg agc cgg gaa gag ctg aag gag ctg gtg 721
Val Ala Glu Ile Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val
225 230 235

aag aaa gca gat gca ggt gag gaa ggt ttg aaa ctg tca cca tgg ttc 769
Lys Lys Ala Asp Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe
240 245 250

aga ttg gtg gtg gac aat ttc ttg atg aag tgg tgg gat cat gta gag 817
Arg Leu Val Val Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu
255 260 265

aaa gga act ttg gtt gaa gct ata gac atg aaa acc atc cac aaa ctc 865
Lys Gly Thr Leu Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
270 275 280

tga acatcttttt tt 880
285

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<210> 96

<211> 284

<212> PRT

<213> Arabidopsis thaliana

<400> 96

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Met Ser Ala Ser Ser Leu Phe Asn Leu Pro Leu Ile Arg Leu Arg Ser
1 5 10 15

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Leu Ala Leu Ser Ser Ser Phe Ser Ser Phe Arg Phe Ala His Arg Pro
20 25 30

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Leu Ser Ser Ile Ser Pro Arg Lys Leu Pro Asn Phe Arg Ala Phe Ser
 35 40 45
 Gly Thr Ala Met Thr Asp Thr Lys Asp Ala Gly Met Asp Ala Val Gln
 50 55 60
 Arg Arg Leu Met Phe Glu Asp Glu Cys Ile Leu Val Asp Glu Thr Asp
 65 70 75 80
 Arg Val Val Gly His Asp Ser Lys Tyr Asn Cys His Leu Met Glu Asn
 85 90 95
 Ile Glu Ala Lys Asn Leu Leu His Arg Ala Phe Ser Val Phe Leu Phe
 100 105 110
 Asn Ser Lys Tyr Glu Leu Leu Leu Gln Gln Arg Ser Asn Thr Lys Val
 115 120 125
 Thr Phe Pro Leu Val Trp Thr Asn Thr Cys Cys Ser His Pro Leu Tyr
 130 135 140
 Arg Glu Ser Glu Leu Ile Gln Asp Asn Ala Leu Gly Val Arg Asn Ala
 145 150 155 160
 Ala Gln Arg Lys Leu Leu Asp Glu Leu Gly Ile Val Ala Glu Asp Val
 165 170 175
 Pro Val Asp Glu Phe Thr Pro Leu Gly Arg Met Leu Tyr Lys Ala Pro
 180 185 190
 Ser Asp Gly Lys Trp Gly Glu His Glu Leu Asp Tyr Leu Leu Phe Ile
 195 200 205
 Val Arg Asp Val Lys Val Gln Pro Asn Pro Asp Glu Val Ala Glu Ile
 210 215 220
 Lys Tyr Val Ser Arg Glu Glu Leu Lys Glu Leu Val Lys Lys Ala Asp
 225 230 235 240
 Ala Gly Glu Glu Gly Leu Lys Leu Ser Pro Trp Phe Arg Leu Val Val
 245 250 255
 Asp Asn Phe Leu Met Lys Trp Trp Asp His Val Glu Lys Gly Thr Leu
 260 265 270
 Val Glu Ala Ile Asp Met Lys Thr Ile His Lys Leu
 275 280

<210> 97

<211> 831

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (18)..(821)

<400> 97

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      Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro
          1              5              10

gcc ttc gcc ggt aag gcc gtc aag ctt tcc ccc gcg gca tca gaa gtc      98
Ala Phe Ala Gly Lys Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val
          15              20              25

ctt gga agc ggc cgt gtg aca atg agg aag act gtt gcc aag cca aag     146
Leu Gly Ser Gly Arg Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys
          30              35              40

ggc cca tca ggc agc cca tgg tac gga tct gac cgt gtc aag tac ttg     194
Gly Pro Ser Gly Ser Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu
          45              50              55

ggc cca ttc tct ggc gaa tca ccg agc tac ctt acc gga gag ttc ccc     242
Gly Pro Phe Ser Gly Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro
          60              65              70              75

gga gac tac gga tgg gac acc gcc gga ctt tca gct gac ccc gag aca     290
Gly Asp Tyr Gly Trp Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr
          80              85              90

ttc gca agg aac cgt gaa cta gaa gtt atc cac agc agg tgg gct atg     338
Phe Ala Arg Asn Arg Glu Leu Glu Val Ile His Ser Arg Trp Ala Met
          95              100              105

ctc gga gcc cta ggc tgc gtc ttc cct gag ctt ttg gct aga aac gga     386
Leu Gly Ala Leu Gly Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly
          110              115              120

gtc aag ttc gga gag gcg gtt tgg ttc aag gcc ggt tca cag atc ttc     434
Val Lys Phe Gly Glu Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe
          125              130              135

agc gat gga ggg ctc gat tac ttg gga aac cct agc ttg gtt cac gct     482
Ser Asp Gly Gly Leu Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala
          140              145              150              155

cag agc att ttg gcc att tgg gcc aca caa gtt att ttg atg gga gcc     530
Gln Ser Ile Leu Ala Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala
          160              165              170

gtt gaa ggc tac aga gtc gca gga aat ggg cca ttg gga gag gcc gag     578
Val Glu Gly Tyr Arg Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu
          175              180              185

gac ttg ctt tac ccc ggt ggc agc ttc gac cca ttg ggt ttg gct acc     626
Asp Leu Leu Tyr Pro Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr
          190              195              200

gac cca gag gca ttc gct gag ttg aag gtg aag gag ctc aag aac gga     674

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Asp Pro Glu Ala Phe Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly
 205                               210                   215

aga ttg gct atg ttc tct atg ttt gga ttc ttc gtt caa gcc atc gtc   722
Arg Leu Ala Met Phe Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val
220                               225                   230                   235

act ggt aag gga ccg ata gag aac ctt gct gac cat ttg gcc gat cca   770
Thr Gly Lys Gly Pro Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro
                240                               245                   250

gtt aac aac aac gca tgg gcc ttc gcc acc aac ttt gtt ccc gga aag   818
Val Asn Asn Asn Ala Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
                255                               260                   265

tga gccaaagtttt                                                    831

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<210> 98
 <211> 267
 <212> PRT
 <213> Arabidopsis thaliana

<400> 98

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Met Ala Ala Ser Thr Met Ala Leu Ser Ser Pro Ala Phe Ala Gly Lys
  1                               5                   10                   15

Ala Val Lys Leu Ser Pro Ala Ala Ser Glu Val Leu Gly Ser Gly Arg
                20                               25                   30

Val Thr Met Arg Lys Thr Val Ala Lys Pro Lys Gly Pro Ser Gly Ser
                35                               40                   45

Pro Trp Tyr Gly Ser Asp Arg Val Lys Tyr Leu Gly Pro Phe Ser Gly
                50                               55                   60

Glu Ser Pro Ser Tyr Leu Thr Gly Glu Phe Pro Gly Asp Tyr Gly Trp
                65                               70                   75                   80

Asp Thr Ala Gly Leu Ser Ala Asp Pro Glu Thr Phe Ala Arg Asn Arg
                85                               90                   95

Glu Leu Glu Val Ile His Ser Arg Trp Ala Met Leu Gly Ala Leu Gly
                100                              105                   110

Cys Val Phe Pro Glu Leu Leu Ala Arg Asn Gly Val Lys Phe Gly Glu
                115                              120                   125

Ala Val Trp Phe Lys Ala Gly Ser Gln Ile Phe Ser Asp Gly Gly Leu
                130                              135                   140

Asp Tyr Leu Gly Asn Pro Ser Leu Val His Ala Gln Ser Ile Leu Ala
                145                              150                   155                   160

Ile Trp Ala Thr Gln Val Ile Leu Met Gly Ala Val Glu Gly Tyr Arg
                165                              170                   175

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Val Ala Gly Asn Gly Pro Leu Gly Glu Ala Glu Asp Leu Leu Tyr Pro
 180 185 190

Gly Gly Ser Phe Asp Pro Leu Gly Leu Ala Thr Asp Pro Glu Ala Phe
 195 200 205

Ala Glu Leu Lys Val Lys Glu Leu Lys Asn Gly Arg Leu Ala Met Phe
 210 215 220

Ser Met Phe Gly Phe Phe Val Gln Ala Ile Val Thr Gly Lys Gly Pro
 225 230 235 240

Ile Glu Asn Leu Ala Asp His Leu Ala Asp Pro Val Asn Asn Asn Ala
 245 250 255

Trp Ala Phe Ala Thr Asn Phe Val Pro Gly Lys
 260 265

<210> 99
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 <212> DNA
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 Met Ala Gly Ile Lys Val Phe Gly His Pro Ala Ser
 1 5 10

aca gcc act aga aga gtt ctc atc gct ctt cac gag aag aat gtc gac 98
 Thr Ala Thr Arg Arg Val Leu Ile Ala Leu His Glu Lys Asn Val Asp
 15 20 25

ttt gaa ttc gtt cat gtc gag ctc aaa gat ggt gaa cac aag aaa gag 146
 Phe Glu Phe Val His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu
 30 35 40

cct ttc atc ctt cgc aac gtgagtacat ataacatctg tcaagccaaa 194
 Pro Phe Ile Leu Arg Asn
 45 50

atattgtatt tcatttagat actgaatctt ggtcttaaca atcttgaata atgtttttgc 254

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ag ccc ttt ggt aaa gtt cca gcc ttt gaa gat gga gac ttc aag att      301
  Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys Ile
                    55                      60                      65

ttc g gtaaatacaa atatatatca ttatagtcac gtttacaaat ttttggtttt      355
Phe G

atgatcattg caataataga aagcagaaac actcaaaaaat gttttttttt tgggtgggcag 415

aa tca aga gca att act caa tac ata gct cat gaa ttc tca gac aaa      462
lu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser Asp Lys
                    70                      75                      80

gga aac aac ctt ctc tca act ggc aag gac atg gcg atc ata gcc atg      510
Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile Ala Met
                    85                      90                      95

ggc att gaa att gag tcg cat gag ttt gac cca gtt ggt tca aag ctt      558
Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser Lys Leu
                    100                     105                     110

gtt tgg gag caa gtc tta aag cct ttg tat ggt atg acc aca gac aaa      606
Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr Asp Lys
                    115                     120                     125

act gtt gtt gaa gaa gaa gag gct aag cta gcc aaa gtc ctc gat gtt      654
Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu Asp Val
                    130                     135                     140                     145

tac gaa cac agg ctt ggt gag tcc aag tat ttg gct tct gac cac ttc      702
Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp His Phe
                    150                     155                     160

act ttg gtc gat ctt cac act atc cct gtg att caa tac tta ctt gga      750
Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu Leu Gly
                    165                     170                     175

act cca act aag aaa ctc ttc gac gag cgt cca cat gtg agt gct tgg      798
Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser Ala Trp
                    180                     185                     190

gtt gct gac atc act tca agg cct tct gct cag aag gtt ctt taa      843
Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
                    195                     200                     205

gtgaatctca aa                                                         855

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<210> 100
 <211> 208
 <212> PRT
 <213> Arabidopsis thaliana

<400> 100
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 1 5 10 15

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      20                      25                      30
His Val Glu Leu Lys Asp Gly Glu His Lys Lys Glu Pro Phe Ile Leu
      35                      40                      45
Arg Asn Pro Phe Gly Lys Val Pro Ala Phe Glu Asp Gly Asp Phe Lys
      50                      55                      60
Ile Phe Glu Ser Arg Ala Ile Thr Gln Tyr Ile Ala His Glu Phe Ser
      65                      70                      75                      80
Asp Lys Gly Asn Asn Leu Leu Ser Thr Gly Lys Asp Met Ala Ile Ile
      85                      90                      95
Ala Met Gly Ile Glu Ile Glu Ser His Glu Phe Asp Pro Val Gly Ser
      100                     105                     110
Lys Leu Val Trp Glu Gln Val Leu Lys Pro Leu Tyr Gly Met Thr Thr
      115                     120                     125
Asp Lys Thr Val Val Glu Glu Glu Glu Ala Lys Leu Ala Lys Val Leu
      130                     135                     140
Asp Val Tyr Glu His Arg Leu Gly Glu Ser Lys Tyr Leu Ala Ser Asp
      145                     150                     155                     160
His Phe Thr Leu Val Asp Leu His Thr Ile Pro Val Ile Gln Tyr Leu
      165                     170                     175
Leu Gly Thr Pro Thr Lys Lys Leu Phe Asp Glu Arg Pro His Val Ser
      180                     185                     190
Ala Trp Val Ala Asp Ile Thr Ser Arg Pro Ser Ala Gln Lys Val Leu
      195                     200                     205

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<210> 101

<211> 512

<212> DNA

<213> Arabidopsis thaliana

<220>

<221> CDS

<222> (12)..(67)

<220>

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<222> (241)..(309)

<220>

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<222> (417)..(492)

<400> 101

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Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln
 1 5 10
 acc gct ggc aaa gct ga ggtactactc tttctctctt tgacagaact 97
 Thr Ala Gly Lys Ala Gl
 15
 cttaaactgg aaaaattggt gaagctataa ctctttgaaa acagttgaaa cttgatcatt 157
 actagaaaatt tcagttactt gtttaattta gtttgctgta attatgtaat tgatgatttt 217
 atgggtacaa tgggtgtcat gta g gag aag agc aat gtt ctg ctg gac aag 268
 u Glu Lys Ser Asn Val Leu Leu Asp Lys
 20 25
 gcc aag gat gct gca gct ggt gct gga gct gga gca caa ca ggtaaacaat 319
 Ala Lys Asp Ala Ala Ala Gly Ala Gly Ala Gln Gl
 30 35 40
 ccatacacag acacataaca tataatatgt aacgaaataa acgtctttgt aagcttacat 379
 gtacgcagat ttctgatatg gttatgtata tggtata g gcg gga aag agt gta 432
 n Ala Gly Lys Ser Val
 45
 tcg gat gcg gca gcg gga ggt gtt aac ttc gtg aag gac aag acc ggc 480
 Ser Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly
 50 55 60
 ctg aac aag tag agattcgggt caaatttggg 512
 Leu Asn Lys
 65

<210> 102
 <211> 66
 <212> PRT
 <213> Arabidopsis thaliana

<400> 102
 Met Ser Glu Thr Asn Lys Asn Ala Phe Gln Ala Gly Gln Thr Ala Gly
 1 5 10 15
 Lys Ala Glu Glu Lys Ser Asn Val Leu Leu Asp Lys Ala Lys Asp Ala
 20 25 30
 Ala Ala Gly Ala Gly Ala Gly Ala Gln Gln Ala Gly Lys Ser Val Ser
 35 40 45
 Asp Ala Ala Ala Gly Gly Val Asn Phe Val Lys Asp Lys Thr Gly Leu
 50 55 60
 Asn Lys
 65

<210> 103
 <211> 1138
 <212> DNA
 <213> Arabidopsis thaliana

<220>
 <221> CDS
 <222> (11)..(1123)

<400> 103
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 Met Ala Thr Leu Val Asp Pro Pro Asn Gly Ile Arg Asn
 1 5 10

gaa ggg aag cat tac ttc tca atg tgg caa act ctg ttc gag atc gac 97
 Glu Gly Lys His Tyr Phe Ser Met Trp Gln Thr Leu Phe Glu Ile Asp
 15 20 25

act aag tac atg cct atc aag cct att ggt cgt gga gct tac ggt gtt 145
 Thr Lys Tyr Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val
 30 35 40 45

gtc tgc tcc tct gtt aac agt gac acc aac gag aaa gtt gct atc aag 193
 Val Cys Ser Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys
 50 55 60

aag att cac aat gtt tat gag aat agg atc gat gcg ttg agg act ctt 241
 Lys Ile His Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu
 65 70 75

cgg gag ctc aag ctt cta cgc cat ctt cga cat gag aat gtc att gct 289
 Arg Glu Leu Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala
 80 85 90

ttg aaa gat gtc atg atg cca att cat aag atg agc ttc aag gat gtt 337
 Leu Lys Asp Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val
 95 100 105

tat ctt gtt tat gag ctc atg gac act gat ctc cac cag att atc aag 385
 Tyr Leu Val Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys
 110 115 120 125

tct tct cag cgt ctt agt aac gat cat tgc caa tac ttc ttg ttc cag 433
 Ser Ser Gln Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln
 130 135 140

ttg ctt cga ggg ctc aag tat att cat tca gcc aat atc ctg cac cga 481
 Leu Leu Arg Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg
 145 150 155

gat ttg aaa cct ggt aac ctt ctt gtc aac gca aac tgc gat tta aag 529
 Asp Leu Lys Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys
 160 165 170

ata tgc gat ttt gga cta gcg cgt gcg agc aac acc aag ggt cag ttc 577
 Ile Cys Asp Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe
 175 180 185

atg act gaa tat gtt gtg act cgt tgg tac cga gcc cca gag ctt ctc 625
 Met Thr Glu Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu
 190 195 200 205
 ctc tgt tgt gac aac tat gga aca tcc att gat gtt tgg tct gtt ggt 673
 Leu Cys Cys Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly
 210 215 220
 tgc att ttc gcc gag ctt ctt ggt agg aaa ccg ata ttc caa gga acg 721
 Cys Ile Phe Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr
 225 230 235
 gaa tgt ctt aac cag ctt aag ctc att gtc aac att atc gga agc caa 769
 Glu Cys Leu Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln
 240 245 250
 aga gaa gaa gat ctt gag ttc ata gtt aac ccg aaa gct aaa aga tac 817
 Arg Glu Glu Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr
 255 260 265
 att aga tca ctt ccg tac tca cct ggg atg tct tta tcc aga ctt tac 865
 Ile Arg Ser Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr
 270 275 280 285
 ccg tgc gct cat gta ttg gcc atc gac ctt ctg cag aaa atg ctt gtt 913
 Pro Cys Ala His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val
 290 295 300
 ttt gat ccg tca aag agg att agt gcc tct gaa gca ctc cag cat cca 961
 Phe Asp Pro Ser Lys Arg Ile Ser Ala Ser Glu Ala Leu Gln His Pro
 305 310 315
 tac atg gcg cca cta tat gac ccg aat gca aac cct cct gct caa gtt 1009
 Tyr Met Ala Pro Leu Tyr Asp Pro Asn Ala Asn Pro Pro Ala Gln Val
 320 325 330
 cct atc gat ctc gat gta gat gag gat ttg aga gag gag atg ata aga 1057
 Pro Ile Asp Leu Asp Val Asp Glu Asp Leu Arg Glu Glu Met Ile Arg
 335 340 345
 gaa atg ata tgg aat gag atg ctt cac tac cat cca caa gct tca acc 1105
 Glu Met Ile Trp Asn Glu Met Leu His Tyr His Pro Gln Ala Ser Thr
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<212> PRT

<213> Arabidopsis thaliana

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Met Pro Ile Lys Pro Ile Gly Arg Gly Ala Tyr Gly Val Val Cys Ser	35	40	45
Ser Val Asn Ser Asp Thr Asn Glu Lys Val Ala Ile Lys Lys Ile His	50	55	60
Asn Val Tyr Glu Asn Arg Ile Asp Ala Leu Arg Thr Leu Arg Glu Leu	65	70	75
Lys Leu Leu Arg His Leu Arg His Glu Asn Val Ile Ala Leu Lys Asp	85	90	95
Val Met Met Pro Ile His Lys Met Ser Phe Lys Asp Val Tyr Leu Val	100	105	110
Tyr Glu Leu Met Asp Thr Asp Leu His Gln Ile Ile Lys Ser Ser Gln	115	120	125
Arg Leu Ser Asn Asp His Cys Gln Tyr Phe Leu Phe Gln Leu Leu Arg	130	135	140
Gly Leu Lys Tyr Ile His Ser Ala Asn Ile Leu His Arg Asp Leu Lys	145	150	155
Pro Gly Asn Leu Leu Val Asn Ala Asn Cys Asp Leu Lys Ile Cys Asp	165	170	175
Phe Gly Leu Ala Arg Ala Ser Asn Thr Lys Gly Gln Phe Met Thr Glu	180	185	190
Tyr Val Val Thr Arg Trp Tyr Arg Ala Pro Glu Leu Leu Leu Cys Cys	195	200	205
Asp Asn Tyr Gly Thr Ser Ile Asp Val Trp Ser Val Gly Cys Ile Phe	210	215	220
Ala Glu Leu Leu Gly Arg Lys Pro Ile Phe Gln Gly Thr Glu Cys Leu	225	230	235
Asn Gln Leu Lys Leu Ile Val Asn Ile Ile Gly Ser Gln Arg Glu Glu	245	250	255
Asp Leu Glu Phe Ile Val Asn Pro Lys Ala Lys Arg Tyr Ile Arg Ser	260	265	270
Leu Pro Tyr Ser Pro Gly Met Ser Leu Ser Arg Leu Tyr Pro Cys Ala	275	280	285
His Val Leu Ala Ile Asp Leu Leu Gln Lys Met Leu Val Phe Asp Pro	290	295	300
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gcg	aag	acg	atg	gct	gct	aac	aag	gac	aaa	gac	aag	gac	aag	aag	aaa	100
Ala	Lys	Thr	Met	Ala	Ala	Asn	Lys	Asp	Lys	Asp	Lys	Asp	Lys	Lys	Lys	
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ccc	atc	tct	cgc	tct	gct	cgt	gct	ggc	att	cag	ttt	cca	gtt	gga	cga	148
Pro	Ile	Ser	Arg	Ser	Ala	Arg	Ala	Gly	Ile	Gln	Phe	Pro	Val	Gly	Arg	
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Ile	His	Arg	Gln	Leu	Lys	Thr	Arg	Val	Ser	Ala	His	Gly	Arg	Val	Gly	
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Ala	Thr	Ala	Ala	Val	Tyr	Thr	Ala	Ser	Ile	Leu	Glu	Tyr	Leu	Thr	Ala	
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gag	gtt	ctt	gag	ttg	gct	ggg	aat	gcg	agc	aag	gat	ctc	aaa	gtg	aag	292
Glu	Val	Leu	Glu	Leu	Ala	Gly	Asn	Ala	Ser	Lys	Asp	Leu	Lys	Val	Lys	
				80					85					90		
agg	ata	acg	cca	agg	cat	ctg	cag	ttg	gcg	att	aga	gga	gat	gag	gag	340
Arg	Ile	Thr	Pro	Arg	His	Leu	Gln	Leu	Ala	Ile	Arg	Gly	Asp	Glu	Glu	
			95					100					105			
ctg	gac	aca	ctc	atc	aag	gga	acg	att	gct	gga	ggc	ggc	gtg	atc	cct	388
Leu	Asp	Thr	Leu	Ile	Lys	Gly	Thr	Ile	Ala	Gly	Gly	Gly	Val	Ile	Pro	
		110					115					120				

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 50 55 60
 Tyr Thr Ala Ser Ile Leu Glu Tyr Leu Thr Ala Glu Val Leu Glu Leu
 65 70 75 80
 Ala Gly Asn Ala Ser Lys Asp Leu Lys Val Lys Arg Ile Thr Pro Arg
 85 90 95
 His Leu Gln Leu Ala Ile Arg Gly Asp Glu Glu Leu Asp Thr Leu Ile
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Tyr Asp Pro Leu His Gln Lys Met Tyr Thr Leu Asn Leu Pro Glu Leu	
15 20 25	
gcc aaa tct acg gtt tgt tac tca aga gat gga tgg tta cta atg cgt	145
Ala Lys Ser Thr Val Cys Tyr Ser Arg Asp Gly Trp Leu Leu Met Arg	
30 35 40	
aaa acc att tca aga gaa atg ttc ttc ttc aac ccg ttt act cgt gag	193
Lys Thr Ile Ser Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu	
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ctc ata aac gta cca aaa tgt act tta tca tat gat gcg atc gct ttc	241
Leu Ile Asn Val Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe	
65 70 75	
tct tgt gca cct aca tca ggt act tgc gtg ttg cta gca ttt aag cat	289
Ser Cys Ala Pro Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His	
80 85 90	
gtt tcg tat cgt atc acc act acg agc act tgc cat ccc aaa gca acc	337
Val Ser Tyr Arg Ile Thr Thr Thr Ser Thr Cys His Pro Lys Ala Thr	
95 100 105	
gag tgg gtt act gag gat cta caa ttc cat cgt cgc ttc cgc agt gaa	385
Glu Trp Val Thr Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu	
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aca ctt aac cac agc aat gtt gtc tat gcc aaa cgt cgc ttc tat tgc	433
Thr Leu Asn His Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys	
125 130 135 140	
ctt gac ggt caa gga agc tta tat tac ttt gat ccg tct tct cga aga	481
Leu Asp Gly Gln Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg	
145 150 155	
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Trp Asp Phe Ser Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp	
160 165 170	
aga ttt agt tac cag tat gag cgg aag aag aag aga att ttc ttg gct	577
Arg Phe Ser Tyr Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala	
175 180 185	
gtg cgg aaa gga gtg ttc ttt aag ata ttt aca tgt gat ggt gag aag	625
Val Arg Lys Gly Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys	
190 195 200	
ccg ata gtg cat aag tta gaa gat atc aat tgg gag gag atc aat agt	673
Pro Ile Val His Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser	
205 210 215 220	
act acg att gat gga ttg aca atc ttt acg ggt ctt tat tcc tct gag	721
Thr Thr Ile Asp Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu	
225 230 235	
gtg aga ctt aat cta cca tgg atg agg aat agt gtt tac ttt cct aga	769

Val Arg Leu Asn Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg
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 Leu Arg Phe Asn Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu
 255 260 265
 agg tat tat ccg cgg aag cag tgg caa gaa cag gag gat tta tgt cct 865
 Arg Tyr Tyr Pro Arg Lys Gln Trp Gln Glu Gln Glu Asp Leu Cys Pro
 270 275 280
 att gag aat ctt tgg att agg cca ccg aag aaa gct gta gat ttc atg 913
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 35 40 45
 Arg Glu Met Phe Phe Phe Asn Pro Phe Thr Arg Glu Leu Ile Asn Val
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 Pro Lys Cys Thr Leu Ser Tyr Asp Ala Ile Ala Phe Ser Cys Ala Pro
 65 70 75 80
 Thr Ser Gly Thr Cys Val Leu Leu Ala Phe Lys His Val Ser Tyr Arg
 85 90 95
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 Glu Asp Leu Gln Phe His Arg Arg Phe Arg Ser Glu Thr Leu Asn His
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 Ser Asn Val Val Tyr Ala Lys Arg Arg Phe Tyr Cys Leu Asp Gly Gln
 130 135 140
 Gly Ser Leu Tyr Tyr Phe Asp Pro Ser Ser Arg Arg Trp Asp Phe Ser
 145 150 155 160
 Tyr Thr Tyr Leu Leu Pro Cys Pro Tyr Ile Ser Asp Arg Phe Ser Tyr
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Gln Tyr Glu Arg Lys Lys Lys Arg Ile Phe Leu Ala Val Arg Lys Gly
 180 185 190
 Val Phe Phe Lys Ile Phe Thr Cys Asp Gly Glu Lys Pro Ile Val His
 195 200 205
 Lys Leu Glu Asp Ile Asn Trp Glu Glu Ile Asn Ser Thr Thr Ile Asp
 210 215 220
 Gly Leu Thr Ile Phe Thr Gly Leu Tyr Ser Ser Glu Val Arg Leu Asn
 225 230 235 240
 Leu Pro Trp Met Arg Asn Ser Val Tyr Phe Pro Arg Leu Arg Phe Asn
 245 250 255
 Val Lys Arg Cys Val Ser Tyr Ser Leu Asp Glu Glu Arg Tyr Tyr Pro
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201

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 Lys Gly Glu Gly Asn Val Ala Tyr Lys Lys Lys Asp Phe Gly Arg Ala
 235 240 245
 gtt gaa cat tat act aag gcc atg gag ctc gat gat gag gat att tcg 939
 Val Glu His Tyr Thr Lys Ala Met Glu Leu Asp Asp Glu Asp Ile Ser
 250 255 260 265
 tat ttg acg aat cgt gct gct gtt tat ctt gag atg ggg aag 981
 Tyr Leu Thr Asn Arg Ala Ala Val Tyr Leu Glu Met Gly Lys
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 Tyr Glu Glu Cys Ile Glu
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 Lys Met Ile Ala Arg Ala Leu Thr Arg Lys Gly Ser Ala Leu Val Lys
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 Lys Ala Leu Thr Glu His Arg Asn Pro Asp Thr Leu Lys Lys Leu Asn
 335 340 345
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 Asp Ala Glu Lys Val Lys Lys Glu Leu Glu Gln Gln Glu Tyr Phe Asp
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 Pro Thr Ile Ala Glu Glu Arg Glu Lys G
 370 375

222

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Cys Val Glu Gln Ile Asn Lys Ala Ser Arg Gly Asp Leu Thr Pro Glu							
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Val Gln Val Arg
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Pro	Thr	Asn	His	Ile	Leu	Tyr	Ser	Asn	Arg	Ser	Ala	Ser	Tyr	Ala	Ser	35	40	45	
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Leu	Lys	Pro	Asp	Trp	Ser	Lys	Gly	Tyr	Ser	Arg	Leu	Gly	Ala	Ala	Phe	65	70	75	80
Ile	Gly	Leu	Ser	Lys	Phe	Asp	Glu	Ala	Val	Asp	Ser	Tyr	Lys	Lys	Gly	85	90	95	
Leu	Glu	Ile	Asp	Pro	Ser	Asn	Glu	Met	Leu	Lys	Ser	Gly	Leu	Ala	Asp	100	105	110	
Ala	Ser	Arg	Ser	Arg	Val	Ser	Ser	Lys	Ser	Asn	Pro	Phe	Val	Asp	Ala	115	120	125	
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Arg	Val	Tyr	Leu	Glu	Gln	Asp	Asp	Phe	Val	Lys	Thr	Met	Lys	Glu	Ile	145	150	155	160
Gln	Arg	Asn	Pro	Asn	Asn	Leu	Asn	Leu	Tyr	Met	Lys	Asp	Lys	Arg	Val	165	170	175	
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Gly	Glu	Asp	Thr	Glu	Met	Lys	Glu	Ala	Asp	Glu	Arg	Lys	Glu	Pro	Glu	195	200	205	
Pro	Glu	Met	Glu	Pro	Met	Glu	Leu	Thr	Glu	Glu	Glu	Arg	Gln	Lys	Lys	210	215	220	
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Thr	Glu	His	Arg	Asn	Pro	Asp	Thr	Leu	Lys	Lys	Leu	Asn	Asp	Ala	Glu
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Lys	Val	Lys	Lys	Glu	Leu	Glu	Gln	Gln	Glu	Tyr	Phe	Asp	Pro	Thr	Ile
		355					360					365			
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	370					375					380				
Tyr	Pro	Glu	Ala	Val	Lys	His	Tyr	Ser	Glu	Ala	Ile	Lys	Arg	Asn	Pro
385					390					395					400
Asn	Asp	Val	Arg	Ala	Tyr	Ser	Asn	Arg	Ala	Ala	Cys	Tyr	Thr	Lys	Leu
			405						410					415	
Gly	Ala	Leu	Pro	Glu	Gly	Leu	Lys	Asp	Ala	Glu	Lys	Cys	Ile	Glu	Leu
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Asp	Pro	Ser	Phe	Thr	Lys	Gly	Tyr	Ser	Arg	Lys	Gly	Ala	Ile	Gln	Phe
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Phe	Met	Lys	Glu	Tyr	Asp	Lys	Ala	Met	Glu	Thr	Tyr	Gln	Glu	Gly	Leu
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Lys	His	Asp	Pro	Lys	Asn	Gln	Glu	Phe	Leu	Asp	Gly	Val	Arg	Arg	Cys
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Val	Glu	Gln	Ile	Asn	Lys	Ala	Ser	Arg	Gly	Asp	Leu	Thr	Pro	Glu	Glu
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Ile	Leu	Ser	Asp	Pro	Val	Met	Arg	Gln	Val	Leu	Val	Asp	Phe	Gln	Glu
		515					520					525			
Asn	Pro	Lys	Ala	Ala	Gln	Glu	His	Met	Lys	Asn	Pro	Met	Val	Met	Asn

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 Met Gly Arg Ala Pro Cys Cys Asp Lys Ala Asn Val Lys Lys
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 ggg cct tgg tct cct gag gaa gac gcc aaa ctc aaa gat tac atc gag 219
 Gly Pro Trp Ser Pro Glu Glu Asp Ala Lys Leu Lys Asp Tyr Ile Glu
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 Asn Ser Gly Thr Gly Gly Asn Trp Ile Ala Leu Pro Gln Lys Ile G
 35 40 45
 gtatgtatta cttaaaactc acttttgatt taaaattggc actgagagtt tccaaatagt 325
 actttgagac cgtgggtcgtg ttaaatttgt gtgttgatga tattttattta catggtatag 385
 gt tta agg aga tgt ggg aag agt tgc agg cta agg tgg ctc aac tat 432
 ly Leu Arg Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr
 50 55 60
 ttg aga cca aac atc aaa cat ggt ggc ttc tcc gag gaa gaa gac aac 480
 Leu Arg Pro Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn
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 atc att tgt aac ctc tat gtt act att ggt agc ag gtactatata 525
 Ile Ile Cys Asn Leu Tyr Val Thr Ile Gly Ser Ar
 80 85

27

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Thr Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala
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gct ttg ggc gga ggg aca acg agt aca tcg gcg gat caa agt aca ata 1408
Ala Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile
                340                345                350

agt tgg gag gat ata act tct cta gtt aat tcc gaa gat gca agt tac 1456
Ser Trp Glu Asp Ile Thr Ser Leu Val Asn Ser Glu Asp Ala Ser Tyr
                355                360                365

ttc aat gcg cca aat cat gtg taa cattttgttt aaaactttat ttgtacttaa 1510
Phe Asn Ala Pro Asn His Val
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Arg Cys Gly Lys Ser Cys Arg Leu Arg Trp Leu Asn Tyr Leu Arg Pro
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Asn Ile Lys His Gly Gly Phe Ser Glu Glu Glu Asp Asn Ile Ile Cys
  65                70                75                80

Asn Leu Tyr Val Thr Ile Gly Ser Arg Trp Ser Ile Ile Ala Ala Gln
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Leu Pro Gly Arg Thr Asp Asn Asp Ile Lys Asn Tyr Trp Asn Thr Arg
                100                105                110

Leu Lys Lys Lys Leu Leu Asn Lys Gln Arg Lys Glu Phe Gln Glu Ala
  115                120                125

Arg Met Lys Gln Glu Met Val Met Met Lys Arg Gln Gln Gln Gly Gln
  130                135                140

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 Phe Gly Ser Ser Pro Trp Pro Leu Leu Pro Gln Leu Pro Pro Pro His
 165 170 175
 His Gln Ile Pro Leu Gly Met Met Glu Pro Thr Ser Cys Asn Tyr Tyr
 180 185 190
 Gln Thr Thr Pro Ser Cys Asn Leu Glu Gln Lys Pro Leu Ile Thr Leu
 195 200 205
 Lys Asn Met Val Lys Ile Glu Glu Glu Gln Glu Arg Thr Asn Pro Asp
 210 215 220
 His His His Gln Asp Ser Val Thr Asn Pro Phe Asp Phe Ser Phe Ser
 225 230 235 240
 Gln Leu Leu Leu Asp Pro Asn Tyr Tyr Leu Gly Ser Gly Gly Gly Gly
 245 250 255
 Glu Gly Asp Phe Ala Ile Met Ser Ser Ser Thr Asn Ser Pro Leu Pro
 260 265 270
 Asn Thr Ser Ser Asp Gln His Pro Ser Gln Gln Gln Glu Ile Leu Gln
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 Trp Phe Gly Ser Ser Asn Phe Gln Thr Glu Ala Ile Asn Asp Met Phe
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 Ile Asn Asn Asn Asn Asn Ile Val Asn Leu Glu Thr Ile Glu Asn Thr
 305 310 315 320
 Lys Val Tyr Gly Asp Ala Ser Val Ala Gly Ala Ala Val Arg Ala Ala
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 Leu Gly Gly Gly Thr Thr Ser Thr Ser Ala Asp Gln Ser Thr Ile Ser
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Gly	His	Met	Lys	Ala	Lys	Leu	Asp	Pro	Leu	Gly	Leu	Glu	Lys	Arg	Glu		
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Ile	Pro	Glu	Asp	Leu	Thr	Pro	Gly	Leu	Tyr	Gly	Phe	Thr	Glu	Ala	Asp		
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ctt	gat	cgg	gaa	ttc	ttt	ctg	ggt	gta	tgg	agg	atg	tcg	ggt	ttt	ctc	583	
Leu	Asp	Arg	Glu	Phe	Phe	Leu	Gly	Val	Trp	Arg	Met	Ser	Gly	Phe	Leu		
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tct	gag	aac	cgc	ccg	gtt	caa	aca	ctg	agg	tcg	ata	ctg	tcg	agg	ctt	631	
Ser	Glu	Asn	Arg	Pro	Val	Gln	Thr	Leu	Arg	Ser	Ile	Leu	Ser	Arg	Leu		
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Glu	Gln	Ala	Tyr	Cys	Gly	Thr	Ile	Gly	Tyr	Glu	Tyr	Met	His	Ile	Ala		
	200					205					210						
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Asp	Arg	Asp	Lys	Cys	Asn	Trp	Leu	Arg	Asp	Lys	Ile	Glu	Thr	Pro	Thr		
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cct	cga	cag	tac	aat	agt	gag	cgt	cgg	atg	gtt	att	tat	gat	agg	ctt	775	
Pro	Arg	Gln	Tyr	Asn	Ser	Glu	Arg	Arg	Met	Val	Ile	Tyr	Asp	Arg	Leu		
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acc	tgg	agc	aca	cag	ttt	gag	aat	ttc	ttg	gct	act	aag	tgg	acc	acg	823	
Thr	Trp	Ser	Thr	Gln	Phe	Glu	Asn	Phe	Leu	Ala	Thr	Lys	Trp	Thr	Thr		
			250					255					260				
gct	aaa	agg	ttt	gga	ctg	gaa	ggt	gct	gaa	tct	ttg	att	cct	ggc	atg	871	
Ala	Lys	Arg	Phe	Gly	Leu	Glu	Gly	Ala	Glu	Ser	Leu	Ile	Pro	Gly	Met		
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aag	gag	atg	ttc	gat	agg	tct	gca	gat	ctc	ggg	gta	gag	aac	ata	gtt	919	
Lys	Glu	Met	Phe	Asp	Arg	Ser	Ala	Asp	Leu	Gly	Val	Glu	Asn	Ile	Val		
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Ile	Gly	Met	Pro	His	Arg	Gly	Arg	Leu	Asn	Val	Leu	Gly	Asn	Val	Val		
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aga	aaa	cct	cta	cgc	caa	ata	ttc	agc	gag	ttt	agc	ggt	ggt	act	agg	1015	
Arg	Lys	Pro	Leu	Arg	Gln	Ile	Phe	Ser	Glu	Phe	Ser	Gly	Gly	Thr	Arg		
				315					320					325			
cca	gta	gat	gaa	gtt	ggg	ctt	tac	acc	gga	aca	ggt	gat	gtg	aaa	tac	1063	
Pro	Val	Asp	Glu	Val	Gly	Leu	Tyr	Thr	Gly	Thr	Gly	Asp	Val	Lys	Tyr		
			330					335					340				
cac	ttg	ggt	aca	tct	tat	gat	cgt	cca	act	aga	gga	ggc	aaa	cat	ctc	1111	
His	Leu	Gly	Thr	Ser	Tyr	Asp	Arg	Pro	Thr	Arg	Gly	Gly	Lys	His	Leu		

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His Leu Ser Leu Val Ala Asn Pro Ser His Leu Glu Ala Val Asp Pro			
360	365	370	
gtt gtg ata ggt aaa acc aga gcg aaa caa tat tac acg aaa gac gag			1207
Val Val Ile Gly Lys Thr Arg Ala Lys Gln Tyr Tyr Thr Lys Asp Glu			
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aac aga aca aag aac atg ggt att ttg atc cat ggg gat ggt agc ttt			1255
Asn Arg Thr Lys Asn Met Gly Ile Leu Ile His Gly Asp Gly Ser Phe			
395	400	405	
gcc gga caa gga gtg gtg tat gaa act ctc cat ctt agt gca ctt cct			1303
Ala Gly Gln Gly Val Val Tyr Glu Thr Leu His Leu Ser Ala Leu Pro			
410	415	420	
aac tac tgt acc ggt gga aca gtg cac att gtg gtg aat aat caa gtg			1351
Asn Tyr Cys Thr Gly Gly Thr Val His Ile Val Val Asn Asn Gln Val			
425	430	435	
gct ttc aca acc gat ccc agg gaa gga agg tct tca cag tat tgc act			1399
Ala Phe Thr Thr Asp Pro Arg Glu Gly Arg Ser Ser Gln Tyr Cys Thr			
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gat gtt gca aag gct ttg agc gcc cca att ttc cat gtc aat gca gat			1447
Asp Val Ala Lys Ala Leu Ser Ala Pro Ile Phe His Val Asn Ala Asp			
455	460	465	470
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Asp Ile Glu Ala Val Val His Ala Cys Glu Leu Ala Ala Glu Trp Arg			
475	480	485	
cag acg ttc cat tct gat gtt gtt gtt gat tta gta tgc tac cgt cgc			1543
Gln Thr Phe His Ser Asp Val Val Val Asp Leu Val Cys Tyr Arg Arg			
490	495	500	
ttt ggg cat aac gag ata gac gaa ccg tca ttc aca caa cca aaa atg			1591
Phe Gly His Asn Glu Ile Asp Glu Pro Ser Phe Thr Gln Pro Lys Met			
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tac aag gtctggctat tatatcatcc atctctgtga aataatctaa taaccaattc			1647
Tyr Lys			
520			
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tggtgatag gtg ata cgc agt cat ccc tcg tca ctt caa atc tac cag gag			1758
Val Ile Arg Ser His Pro Ser Ser Leu Gln Ile Tyr Gln Glu			
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Lys Leu Leu Gln Ser Gly Gln Val Thr Gln Glu Asp Ile Asp Lys Ile			
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 Phe Lys Ser Pro Glu Gln Ile Ser Arg Ile Arg Asn Thr Gl
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 cca cac aga gga gtt aaa aga gtt tat gaa caa cgt gct caa atg att 2163
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 Ala Thr Leu Val Val Glu Gly Asn His Val Arg Leu Ser Gly Gln Asp
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 Val Glu Arg Gly Thr Phe Ser His Arg His Ser Val Leu His Asp Gln
 670 675 680
 gaa acc ggg gag gaa tat tgt ccc ctc gat cac cta atc aaa aac caa 2355
 Glu Thr Gly Glu Glu Tyr Cys Pro Leu Asp His Leu Ile Lys Asn Gln
 685 690 695
 gac cct gaa atg ttc act gtc agc aac ag gtagcattt ttttttaatc 2404
 Asp Pro Glu Met Phe Thr Val Ser Asn Se
 700 705
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 cag c tcc ctt tca gaa ttt ggt gtt ctc ggt ttc gaa ctg ggt tat tcg 2513
 r Ser Leu Ser Glu Phe Gly Val Leu Gly Phe Glu Leu Gly Tyr Se
 710 715 720
 atg gaa aat ccc aat tct ctg gtg ata tgg gaa gct cag ttt gga gac 2561
 r Met Glu Asn Pro Asn Ser Leu Val Ile Trp Glu Ala Gln Phe Gly As
 725 730 735
 ttt gct aat ggc gca caa gtt atg ttt gat cag ttc ata agc agt ggg 2609
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755              760              765              770
gga tat gat ggt cag ggt cct gaa cat tcc agt gga aga ttg gaa cgt 2705
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775              780              785
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g Phe Leu Gln
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Met Ser Asp As
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aat cct tac gtt atc cct gag atg gac cca act ctt cga aag cag att 2859
p Asn Pro Tyr Val Ile Pro Glu Met Asp Pro Thr Leu Arg Lys Gln Il
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810              815              820              825
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Ile His Arg Asp Phe Arg Lys Pro Leu Ile Val Met Ala Pro Lys As
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p Val Lys Gly His Pro Gly Phe Asp Lys Gln Gly Thr Arg Phe Lys Ar
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885              890
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          35           40           45
Lys Ala Glu Ser Ala Ala Pro Val Pro Arg Pro Val Pro Leu Ser Lys
          50           55           60
Leu Thr Asp Ser Phe Leu Asp Gly Thr Ser Ser Val Tyr Leu Glu Glu
  65           70           75           80
Leu Gln Arg Ala Trp Glu Ala Asp Pro Asn Ser Val Asp Glu Ser Trp
          85           90           95
Asp Asn Phe Phe Arg Asn Phe Val Gly Gln Ala Ser Thr Ser Pro Gly
          100          105          110
Ile Ser Gly Gln Thr Ile Gln Glu Ser Met Arg Leu Leu Leu Leu Val
          115          120          125
Arg Ala Tyr Gln Val Asn Gly His Met Lys Ala Lys Leu Asp Pro Leu
          130          135          140

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Gly Leu Glu Lys Arg Glu Ile Pro Glu Asp Leu Thr Pro Gly Leu Tyr
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 Phe Gly Ap Phe Ala Asn Gly Ala Gln Val Met Phe Asp Gln Phe Ile
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Val	Val	Asn	Val	Thr	Thr	Pro	Ala	Asn	Trp	Phe	His	Val	Leu	Arg	Arg
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Asp	Val	Lys	Gly	His	Pro	Gly	Phe	Asp	Lys	Gln	Gly	Thr	Arg	Phe	Lys
					860					865					870
Arg	Leu	Ile	Lys	Asp	Gln	Ser	Gly	His	Ser	Asp	Leu	Glu	Glu		
					875					880					885
Asp	Ala	Glu	Ile	Val	Trp	Cys	Gln	Glu	Glu	Pro	Met	Asn	Met	Gly	Gly
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Tyr	Gln	Tyr	Ile	Ala	Leu	Arg	Leu	Cys	Thr	Ala	Met	Lys	Ala	Leu	Gln
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Arg	Gly	Asn	Phe	Asn	Asp	Ile	Lys	Tyr	Val	Gly	Arg	Leu	Pro	Ser	Ala
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Ala	Thr	Ala	Thr	Gly	Phe	Tyr	Gln	Leu	His	Val	Lys	Glu	Gln	Thr	Asp
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Ala Thr Phe Val Glu Asp Phe Lys Ala Ala Trp Ser Glu Ser His Ile
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cgt caa atg gaa gac gga aaa gct atc cag ctc gtc ctt gat cag agc      147
Arg Gln Met Glu Asp Gly Lys Ala Ile Gln Leu Val Leu Asp Gln Ser
          30           35           40

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Thr G

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                               ly

tgt gga ttt gct tcc aaa aga aaa tat cta ttc gga cga gtg agc atg      306
Cys Gly Phe Ala Ser Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met
 45           50           55

aag atc aaa ctc att ccc gga gac tct gcc ggt acg gtc acc gct ttc      354
Lys Ile Lys Leu Ile Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe
 60           65           70           75

tac gtaagtctat catttttact cactagtttt gaaattttac acattcacac      407
Tyr

aataaaaaaat aacatttttct tgaaacacta acgggtcaaatt cattgatatg tctatag      464

atg aac tcc gat acg gcc acg gtg aga gac gag cta gat ttt gag ttc      512
Met Asn Ser Asp Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe
          80           85           90

ttg gga aac aga agt ggt caa cct tac tca gtg caa aca aac ata ttt      560
Leu Gly Asn Arg Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe
          95           100          105

gct cat ggc aaa gga gat aga gaa caa aga gtt aat ctt tgg ttc gac      608
Ala His Gly Lys Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp
 110           115           120

cca tct atg gat tac cac act tac act atc tta tgg tca cac aaa cac      656
Pro Ser Met Asp Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His
 125           130           135           140

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att gtg taagcttttc tctaattgta ctttcaacta gaatcaacat ttactgtttc 712
Ile Val

aaaacaaaaa atcaccatatt actgttttaaa aaaaccttag tttaacgtgg gggtgttttg 772

gttactcagt ttt tac gta gac gat gtg cca ata aga gaa tac aaa aac 821
Phe Tyr Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn
145 150 155

aac gaa gcc aag aac ata gct tac cca aca tca caa cct atg gga gta 869
Asn Glu Ala Lys Asn Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val
160 165 170

tac tca aca tta tgg gaa gca gat gac tgg gca aca cgt ggt gga tta 917
Tyr Ser Thr Leu Trp Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu
175 180 185

gag aaa att gat tgg agc aaa gct cca ttt tat gct tat tac aaa gat 965
Glu Lys Ile Asp Trp Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp
190 195 200

ttc gac atc gaa ggt tgt cct gtt cct gga cca acc ttt tgt cca tcg 1013
Phe Asp Ile Glu Gly Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser
205 210 215

aac cct cat aat tgg tgg gaa ggt tat gcc tat cag tct ctt aac gcc 1061
Asn Pro His Asn Trp Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala
220 225 230 235

gtt gaa gct cga cgt tac cgg tgg gtt aga gta aac cat atg gtt tat 1109
Val Glu Ala Arg Arg Tyr Arg Trp Val Arg Val Asn His Met Val Tyr
240 245 250

gat tat tgt act gac cgg tct agg ttt cct gtc cca cca ccc gag tgt 1157
Asp Tyr Cys Thr Asp Arg Ser Arg Phe Pro Val Pro Pro Pro Glu Cys
255 260 265

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Arg Ala
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Ala Ile Gln Leu Val Leu Asp Gln Ser Thr Gly Cys Gly Phe Ala Ser
35 40 45

Lys Arg Lys Tyr Leu Phe Gly Arg Val Ser Met Lys Ile Lys Leu Ile
 50 55 60
 Pro Gly Asp Ser Ala Gly Thr Val Thr Ala Phe Tyr Met Asn Ser Asp
 65 70 75 80
 Thr Ala Thr Val Arg Asp Glu Leu Asp Phe Glu Phe Leu Gly Asn Arg
 85 90 95
 Ser Gly Gln Pro Tyr Ser Val Gln Thr Asn Ile Phe Ala His Gly Lys
 100 105 110
 Gly Asp Arg Glu Gln Arg Val Asn Leu Trp Phe Asp Pro Ser Met Asp
 115 120 125
 Tyr His Thr Tyr Thr Ile Leu Trp Ser His Lys His Ile Val Phe Tyr
 130 135 140
 Val Asp Asp Val Pro Ile Arg Glu Tyr Lys Asn Asn Glu Ala Lys Asn
 145 150 155 160
 Ile Ala Tyr Pro Thr Ser Gln Pro Met Gly Val Tyr Ser Thr Leu Trp
 165 170 175
 Glu Ala Asp Asp Trp Ala Thr Arg Gly Gly Leu Glu Lys Ile Asp Trp
 180 185 190
 Ser Lys Ala Pro Phe Tyr Ala Tyr Tyr Lys Asp Phe Asp Ile Glu Gly
 195 200 205
 Cys Pro Val Pro Gly Pro Thr Phe Cys Pro Ser Asn Pro His Asn Trp
 210 215 220
 Trp Glu Gly Tyr Ala Tyr Gln Ser Leu Asn Ala Val Glu Ala Arg Arg
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 Tyr Arg Trp Val Arg Val Asn His Met Val Tyr Asp Tyr Cys Thr Asp
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Ile Arg Arg Thr Leu Thr Lys Pro His Gly Thr Phe Ser Arg Cys Arg
 10                      15                      20                      25

tac tta tca acc gcc gct gct gcg acg gag gtg aat tac gag gat gaa      147
Tyr Leu Ser Thr Ala Ala Ala Thr Glu Val Asn Tyr Glu Asp Glu
                      30                      35                      40

tcg att atg atg aaa gga gtt cga att tca ggt aga cct ctt tac tta      195
Ser Ile Met Met Lys Gly Val Arg Ile Ser Gly Arg Pro Leu Tyr Leu
                      45                      50                      55

gat atg caa gcg acg act ccg att gat cct aga gta ttc gat gcg atg      243
Asp Met Gln Ala Thr Thr Pro Ile Asp Pro Arg Val Phe Asp Ala Met
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aat gct tca cag atc cat gag tat ggg aat cct cac tcg cga acg cat      291
Asn Ala Ser Gln Ile His Glu Tyr Gly Asn Pro His Ser Arg Thr His
                      75                      80                      85

ctc tac ggc tgg gaa gct gag aac gcc gtc gag aac gca cga aac cag      339
Leu Tyr Gly Trp Glu Ala Glu Asn Ala Val Glu Asn Ala Arg Asn Gln
 90                      95                      100                      105

gtc gcg aaa ctg atc gaa gct tca ccg aag gag atc gta ttc gtg tcc      387
Val Ala Lys Leu Ile Glu Ala Ser Pro Lys Glu Ile Val Phe Val Ser
                      110                      115                      120

ggg gca acg gag gcg aac aat atg gcg gtg aaa gga gtg atg cac ttt      435
Gly Ala Thr Glu Ala Asn Asn Met Ala Val Lys Gly Val Met His Phe
                      125                      130                      135

tac aag gac acg aag aaa cat gtg ata act aca cag act gag cat aag      483
Tyr Lys Asp Thr Lys Lys His Val Ile Thr Thr Gln Thr Glu His Lys
                      140                      145                      150

tgt gtg ctt gat tcg tgt agg cat ttg cag caa gaa gga ttt gag gta      531
Cys Val Leu Asp Ser Cys Arg His Leu Gln Gln Glu Gly Phe Glu Val
                      155                      160                      165

act tat tta cct gtg aaa act gat gga ttg gtt gat tta gag atg ttg      579
Thr Tyr Leu Pro Val Lys Thr Asp Gly Leu Val Asp Leu Glu Met Leu
                      170                      175                      180                      185

aga gaa gct att agg cca gac aca ggg cta gtt tct att atg gct gtg      627
Arg Glu Ala Ile Arg Pro Asp Thr Gly Leu Val Ser Ile Met Ala Val
                      190                      195                      200

aac aat gag att ggt gtg gtt caa cct atg gag gag att ggt atg att      675
Asn Asn Glu Ile Gly Val Val Gln Pro Met Glu Glu Ile Gly Met Ile
                      205                      210                      215

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tgc aaa gag cat aat gtt ccg ttt cat act gat gct gct caa gct att	723
Cys Lys Glu His Asn Val Pro Phe His Thr Asp Ala Ala Gln Ala Ile	
220 225 230	
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Gly Lys Ile Pro Val Asp Val Lys Lys Trp Asn Val Ala Leu Met Ser	
235 240 245	
atg agt gct cac aag atc tat gga ccg aaa ggt gtt ggt gct ttg tat	819
Met Ser Ala His Lys Ile Tyr Gly Pro Lys Gly Val Gly Ala Leu Tyr	
250 255 260 265	
gtg agg agg agg ccg aga atc agg ctt gag ccg ttg atg aat ggt gga	867
Val Arg Arg Arg Pro Arg Ile Arg Leu Glu Pro Leu Met Asn Gly Gly	
270 275 280	
ggt cag gag agg gga ttg cgt agt ggt acg ggg gct acg cag cag att	915
Gly Gln Glu Arg Gly Leu Arg Ser Gly Thr Gly Ala Thr Gln Gln Ile	
285 290 295	
gtt ggg ttc ggg gct gct tgt gag ttg gct atg aag gag atg gag tat	963
Val Gly Phe Gly Ala Ala Cys Glu Leu Ala Met Lys Glu Met Glu Tyr	
300 305 310	
gat gag aag tgg att aag ggg tta cag gag agg ttg ctg aat ggg gtt	1011
Asp Glu Lys Trp Ile Lys Gly Leu Gln Glu Arg Leu Leu Asn Gly Val	
315 320 325	
aga gag aag ctt gat ggt gtt gtg gtg aat ggt tca atg gat agt cga	1059
Arg Glu Lys Leu Asp Gly Val Val Val Asn Gly Ser Met Asp Ser Arg	
330 335 340 345	
tat gta ggg aat ttg aat ttg tcg ttt gct tat gtt gaa gga gag agt	1107
Tyr Val Gly Asn Leu Asn Leu Ser Phe Ala Tyr Val Glu Gly Glu Ser	
350 355 360	
ttg ttg atg gga ttg aag gaa gtt gca gtg tct agt gga agt gct tgt	1155
Leu Leu Met Gly Leu Lys Glu Val Ala Val Ser Ser Gly Ser Ala Cys	
365 370 375	
act agt gcg agt ttg gag cct tct tat gtg ttg aga gct ttg ggt gtg	1203
Thr Ser Ala Ser Leu Glu Pro Ser Tyr Val Leu Arg Ala Leu Gly Val	
380 385 390	
gat gaa gac atg gct cac act tcg att agg ttt ggg att ggt agg ttt	1251
Asp Glu Asp Met Ala His Thr Ser Ile Arg Phe Gly Ile Gly Arg Phe	
395 400 405	
acc acg aag gaa gag att gat aaa gcg gtc gag ctt acg gtt aaa caa	1299
Thr Thr Lys Glu Glu Ile Asp Lys Ala Val Glu Leu Thr Val Lys Gln	
410 415 420 425	
gtt gag aag ttg agg gaa atg agc ccg ctt tat gaa atg gtt aaa gaa	1347
Val Glu Lys Leu Arg Glu Met Ser Pro Leu Tyr Glu Met Val Lys Glu	
430 435 440	
ggt atc gat atc aag aac att caa tgg tct caa cac tga ttcaacagtt	1396

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1399

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 35 40 45

Arg Ile Ser Gly Arg Pro Leu Tyr Leu Asp Met Gln Ala Thr Thr Pro
 50 55 60

Ile Asp Pro Arg Val Phe Asp Ala Met Asn Ala Ser Gln Ile His Glu
 65 70 75 80

Tyr Gly Asn Pro His Ser Arg Thr His Leu Tyr Gly Trp Glu Ala Glu
 85 90 95

Asn Ala Val Glu Asn Ala Arg Asn Gln Val Ala Lys Leu Ile Glu Ala
 100 105 110

Ser Pro Lys Glu Ile Val Phe Val Ser Gly Ala Thr Glu Ala Asn Asn
 115 120 125

Met Ala Val Lys Gly Val Met His Phe Tyr Lys Asp Thr Lys Lys His
 130 135 140

Val Ile Thr Thr Gln Thr Glu His Lys Cys Val Leu Asp Ser Cys Arg
 145 150 155 160

His Leu Gln Gln Glu Gly Phe Glu Val Thr Tyr Leu Pro Val Lys Thr
 165 170 175

Asp Gly Leu Val Asp Leu Glu Met Leu Arg Glu Ala Ile Arg Pro Asp
 180 185 190

Thr Gly Leu Val Ser Ile Met Ala Val Asn Asn Glu Ile Gly Val Val
 195 200 205

Gln Pro Met Glu Glu Ile Gly Met Ile Cys Lys Glu His Asn Val Pro
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Phe His Thr Asp Ala Ala Gln Ala Ile Gly Lys Ile Pro Val Asp Val
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	1				5					10						
ctt	ctt	tct	tgt	ttt	ctc	caa	ggt	tct	tcc	aat	gga	gac	gct	gag	ata	97
Leu	Leu	Ser	Cys	Phe	Leu	Gln	Val	Ser	Ser	Asn	Gly	Asp	Ala	Glu	Ile	
15					20					25					30	
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Leu	Ser	Arg	Val	Lys	Lys	Thr	Arg	Leu	Phe	Asp	Pro	Asp	Gly	Asn	Leu	
				35					40					45		
caa	gat	tgg	gtc	ata	acc	gga	gat	aat	cgg	agt	cca	tgt	aat	tgg	acg	193
Gln	Asp	Trp	Val	Ile	Thr	Gly	Asp	Asn	Arg	Ser	Pro	Cys	Asn	Trp	Thr	
			50					55					60			
gga	atc	aca	tgc	cac	atc	aga	aaa	ggt	agc	tcc	ctc	gcc	gtc	act	acc	241
Gly	Ile	Thr	Cys	His	Ile	Arg	Lys	Gly	Ser	Ser	Leu	Ala	Val	Thr	Thr	
	65						70					75				
att	gat	ctc	tcc	ggc	tat	aat	atc	tcc	ggt	ggc	ttt	ccc	tac	gga	ttc	289
Ile	Asp	Leu	Ser	Gly	Tyr	Asn	Ile	Ser	Gly	Gly	Phe	Pro	Tyr	Gly	Phe	
	80					85					90					
tgt	cgt	atc	cgt	aca	ctc	atc	aac	atc	act	ctt	tct	caa	aac	aat	ctc	337
Cys	Arg	Ile	Arg	Thr	Leu	Ile	Asn	Ile	Thr	Leu	Ser	Gln	Asn	Asn	Leu	
95					100					105					110	
aat	ggt	acg	att	gat	tct	gct	cct	ctc	tcc	ctc	tgt	tct	aaa	ctt	cag	385
Asn	Gly	Thr	Ile	Asp	Ser	Ala	Pro	Leu	Ser	Leu	Cys	Ser	Lys	Leu	Gln	
				115				120						125		
aat	ttg	att	ctc	aat	caa	aac	aac	ttc	tcc	ggt	aaa	tta	ccg	gaa	ttc	433
Asn	Leu	Ile	Leu	Asn	Gln	Asn	Asn	Phe	Ser	Gly	Lys	Leu	Pro	Glu	Phe	
			130					135					140			
tca	ccg	gag	ttt	cgt	aaa	tta	cga	gtc	ctc	gaa	ttg	gaa	tca	aac	ctc	481
Ser	Pro	Glu	Phe	Arg	Lys	Leu	Arg	Val	Leu	Glu	Leu	Glu	Ser	Asn	Leu	
		145					150					155				
ttc	acc	ggt	gag	att	cct	caa	agt	tac	ggg	aga	ctc	act	gct	ctg	caa	529
Phe	Thr	Gly	Glu	Ile	Pro	Gln	Ser	Tyr	Gly	Arg	Leu	Thr	Ala	Leu	Gln	
	160					165					170					
ggt	ctg	aat	ctt	aat	ggt	aac	ccg	ctc	agt	gga	atc	ggt	ccg	gcg	ttt	577
Val	Leu	Asn	Leu	Asn	Gly	Asn	Pro	Leu	Ser	Gly	Ile	Val	Pro	Ala	Phe	
175					180					185					190	
ttg	ggt	tat	ctg	act	gag	tta	act	cgt	ctt	gat	ctc	gct	tac	atc	agt	625
Leu	Gly	Tyr	Leu	Thr	Glu	Leu	Thr	Arg	Leu	Asp	Leu	Ala	Tyr	Ile	Ser	
				195					200					205		

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Phe Asp Pro Ser Pro Ile Pro Ser Thr Leu Gly Asn Leu Ser Asn Leu	
210 215 220	
act gat ctt cgg cta act cac tcg aac ctc gtc gga gaa att cct gat	721
Thr Asp Leu Arg Leu Thr His Ser Asn Leu Val Gly Glu Ile Pro Asp	
225 230 235	
tcg atc atg aat ctg gtg ttg tta gag aat ctt gat tta gct atg aat	769
Ser Ile Met Asn Leu Val Leu Leu Glu Asn Leu Asp Leu Ala Met Asn	
240 245 250	
agt ctc acc gga gaa ata cct gag agt atc gga aga ctc gaa tcg gtt	817
Ser Leu Thr Gly Glu Ile Pro Glu Ser Ile Gly Arg Leu Glu Ser Val	
255 260 265 270	
tac cag att gag ctc tac gat aac cgg tta tct gga aaa tta ccg gag	865
Tyr Gln Ile Glu Leu Tyr Asp Asn Arg Leu Ser Gly Lys Leu Pro Glu	
275 280 285	
agt atc gga aat tta acc gaa ttg agg aat ttt gat gtc tcg cag aat	913
Ser Ile Gly Asn Leu Thr Glu Leu Arg Asn Phe Asp Val Ser Gln Asn	
290 295 300	
aat cta acc ggt gaa cta ccg gaa aag atc gct gct ctg caa ctt atc	961
Asn Leu Thr Gly Glu Leu Pro Glu Lys Ile Ala Ala Leu Gln Leu Ile	
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320 325 330	
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355 360 365	
gaa ttc gat gtc tcg acg aac aga ttc tcc ggt gaa ttg ccg ccg tat	1153
Glu Phe Asp Val Ser Thr Asn Arg Phe Ser Gly Glu Leu Pro Pro Tyr	
370 375 380	
ttg tgc tac aga aga aaa ctt cag aag att atc acc ttc agc aat caa	1201
Leu Cys Tyr Arg Arg Lys Leu Gln Lys Ile Ile Thr Phe Ser Asn Gln	
385 390 395	
tta agc ggc gaa att ccg gaa tct tac ggc gat tgt cat tcg ctt aat	1249
Leu Ser Gly Glu Ile Pro Glu Ser Tyr Gly Asp Cys His Ser Leu Asn	
400 405 410	
tac att cgt atg gcg gat aac aaa ctc tcc ggc gaa gtt ccg gct agg	1297
Tyr Ile Arg Met Ala Asp Asn Lys Leu Ser Gly Glu Val Pro Ala Arg	
415 420 425 430	
ttt tgg gaa ctt cct ctt act cgt ctt gag cta gcc aac aac aat caa	1345

Phe Trp Glu Leu Pro Leu Thr Arg Leu Glu Leu Ala Asn Asn Asn Gln	
435 440 445	
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450 455 460	
cag ctt gaa atc tcc gct aac aac ttc tcc ggt gtg att ccc gtc aaa	1441
Gln Leu Glu Ile Ser Ala Asn Asn Phe Ser Gly Val Ile Pro Val Lys	
465 470 475	
ctt tgt gat ctc cgt gat ctc aga gtc atc gat ctt agc cgc aac agt	1489
Leu Cys Asp Leu Arg Asp Leu Arg Val Ile Asp Leu Ser Arg Asn Ser	
480 485 490	
ttc tta gga tca att ccg tct tgc atc aac aaa ttg aag aat cta gag	1537
Phe Leu Gly Ser Ile Pro Ser Cys Ile Asn Lys Leu Lys Asn Leu Glu	
495 500 505 510	
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Arg Val Glu Met Gln Glu Asn Met Leu Asp Gly Glu Ile Pro Ser Ser	
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Val Ser Ser Cys Thr Glu Leu Thr Glu Leu Asn Leu Ser Asn Asn Arg	
530 535 540	
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Tyr Leu Asp Leu Ser Asn Asn Gln Leu Thr Gly Glu Ile Pro Ala Glu	
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Tyr G ly	
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Asn Pro Asn Leu Cys Ala Pro Asn Leu Asp Pro Ile Arg Pro Cys Arg	
595 600 605	
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Ser Lys Arg Glu Thr Arg Tyr Ile Leu Pro Ile Ser Ile Leu Cys Ile	
610 615 620	
gtt gca cta acc gga gct ttg gtt tgg cta ttc atc aaa acc aaa ccg	1978
Val Ala Leu Thr Gly Ala Leu Val Trp Leu Phe Ile Lys Thr Lys Pro	
625 630 635 640	
tta ttc aag aga aaa ccg aaa cgg acc aac aaa ata acc atc ttc cag	2026
Leu Phe Lys Arg Lys Pro Lys Arg Thr Asn Lys Ile Thr Ile Phe Gln	
645 650 655	

229

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 860 865 870

gaa ctg att acg gga aaa aga ccg aac gat tcg tct ttt ggg gag aat 2809
 Glu Leu Ile Thr Gly Lys Arg Pro Asn Asp Ser Ser Phe Gly Glu Asn
 875 880 885

aag gac att gtt aag ttt gca atg gaa gca gct ttg tgt tac cct tct 2857
 Lys Asp Ile Val Lys Phe Ala Met Glu Ala Ala Leu Cys Tyr Pro Ser
 890 895 900

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 Pro Ser Ala Glu Asp Gly Ala Met Asn Gln Asp Ser Leu Gly Asn Tyr
 905 910 915 920

cga gat ctt agc aag ctt gtt gat cca aag atg aaa ctt tcg acg aga 2953
 Arg Asp Leu Ser Lys Leu Val Asp Pro Lys Met Lys Leu Ser Thr Arg
 925 930 935

gag tat gaa gag ata gag aaa gtt ctt gac gtt gca ttg ctc tgt acg 3001
 Glu Tyr Glu Glu Ile Glu Lys Val Leu Asp Val Ala Leu Leu Cys Thr
 940 945 950

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 Ser Ser Phe Pro Ile Asn Arg Pro Thr Met Arg Lys Val Val Glu Leu
 955 960 965

ctt aaa gag aag aaa tca cta gag tga tattaatcct aggcttttaa 3096
 Leu Lys Glu Lys Lys Ser Leu Glu
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 20 25 30

Arg Val Lys Lys Thr Arg Leu Phe Asp Pro Asp Gly Asn Leu Gln Asp
 35 40 45

Trp Val Ile Thr Gly Asp Asn Arg Ser Pro Cys Asn Trp Thr Gly Ile
 50 55 60

Thr Cys His Ile Arg Lys Gly Ser Ser Leu Ala Val Thr Thr Ile Asp
 65 70 75 80

Leu Ser Gly Tyr Asn Ile Ser Gly Gly Phe Pro Tyr Gly Phe Cys Arg
 85 90 95
 Ile Arg Thr Leu Ile Asn Ile Thr Leu Ser Gln Asn Asn Leu Asn Gly
 100 105 110
 Thr Ile Asp Ser Ala Pro Leu Ser Leu Cys Ser Lys Leu Gln Asn Leu
 115 120 125
 Ile Leu Asn Gln Asn Asn Phe Ser Gly Lys Leu Pro Glu Phe Ser Pro
 130 135 140
 Glu Phe Arg Lys Leu Arg Val Leu Glu Leu Glu Ser Asn Leu Phe Thr
 145 150 155 160
 Gly Glu Ile Pro Gln Ser Tyr Gly Arg Leu Thr Ala Leu Gln Val Leu
 165 170 175
 Asn Leu Asn Gly Asn Pro Leu Ser Gly Ile Val Pro Ala Phe Leu Gly
 180 185 190
 Tyr Leu Thr Glu Leu Thr Arg Leu Asp Leu Ala Tyr Ile Ser Phe Asp
 195 200 205
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INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁷ : C12N 15/82, 15/10, 9/12, 5/10, C12Q 1/68, A01H 5/00	A3	(11) International Publication Number: WO 00/08187 (43) International Publication Date: 17 February 2000 (17.02.00)
(21) International Application Number: PCT/EP99/05652 (22) International Filing Date: 4 August 1999 (04.08.99) (30) Priority Data: 98202634.6 4 August 1998 (04.08.98) EP (71) Applicant (for all designated States except US): VLAAMS INTERUNIVERSITAIR INSTITUUT VOOR BIOTECH- NOLOGIE [BE/BE]; Rijvisschestraat 120, B-9052 Zwij- naarde (BE). (72) Inventors; and (75) Inventors/Applicants (for US only): LEE, Jeong, Hee [KR/BE]; Spinnolenplein 274 (22K), B-9000 Gent (BE). VERBRUGGEN, Nathalie [BE/BE]; Avenue des Saisons, 53, B-1050 Ixelles (BE). (74) Agent: DE CLERCQ, Ann; Ann De Clercq & Co. B.V.B.A., Brandstraat 100, B-9830 Sint-Martens-Latem (BE).		(81) Designated States: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>With international search report.</i> (88) Date of publication of the international search report: 29 June 2000 (29.06.00)
(54) Title: GENES INVOLVED IN TOLERANCE TO ENVIRONMENTAL STRESS		
(57) Abstract <p>The present invention relates to a method for obtaining polynucleic acids comprising coding sequences and/or genes involved in environmental stress resistance in plants, comprising the preparation of a cDNA library comprising coding sequences from siliques, introducing said coding sequences in yeast cells in a functional format and screening for polynucleic acids leading to an enhanced tolerance or resistance to environmental stress conditions in said transformed yeast cells. The present invention further relates to an isolated polynucleic acid obtainable by such a method as listed in Table 1 as well as recombinant polynucleic acid comprising the same. The present invention further relates to an isolated polypeptide encoded by a polynucleic acid of the invention. The present invention also relates to a method for producing a plant with enhanced tolerance or resistance to environmental stress, said method comprising introducing into a plant cell a recombinant DNA comprising a polynucleic acid as defined which when expressed in a plant cell enhances the tolerances or induces resistance to environmental stress conditions of said plant. The present invention particularly relates to plant cells, plants or harvestable parts or propagation material thereof transformed with a recombinant polynucleic acid as defined above.</p>		

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DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

INTERNATIONAL SEARCH REPORT

International Application No
PCT/EP 99/05652

A. CLASSIFICATION OF SUBJECT MATTER IPC 7 C12N15/82 C12N15/10 C12N9/12 C12N5/10 C12Q1/68 A01H5/00		
According to International Patent Classification (IPC) or to both national classification and IPC		
B. FIELDS SEARCHED Minimum documentation searched (classification system followed by classification symbols) IPC 7 C12N		
Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched		
Electronic data base consulted during the international search (name of data base and, where practical, search terms used)		
C. DOCUMENTS CONSIDERED TO BE RELEVANT		
Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	PRÄNDL, R., ET AL. : "HSF3, a new heat shock factor from Arabidopsis thaliana, derepresses the heat shock response and confers thermotolerance when overexpressed in transgenic plants" MOLECULAR AND GENERAL GENETICS, vol. 258, May 1998 (1998-05), pages 269-278, XP002135096 the whole document <div style="text-align: center; margin-top: 10px;">--- -/--</div>	2,3,7,8, 11-14, 16,18, 21, 24-26, 28-37
<div style="display: flex; justify-content: space-between;"> <input checked="" type="checkbox"/> Further documents are listed in the continuation of box C. <input checked="" type="checkbox"/> Patent family members are listed in annex. </div>		
<div style="display: flex;"> <div style="flex: 1;"> <p>° Special categories of cited documents :</p> <p>"A" document defining the general state of the art which is not considered to be of particular relevance</p> <p>"E" earlier document but published on or after the international filing date</p> <p>"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)</p> <p>"O" document referring to an oral disclosure, use, exhibition or other means</p> <p>"P" document published prior to the international filing date but later than the priority date claimed</p> </div> <div style="flex: 1;"> <p>"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention</p> <p>"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone</p> <p>"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.</p> <p>"&" document member of the same patent family</p> </div> </div>		
Date of the actual completion of the international search <div style="text-align: center; font-size: 1.2em;">10 April 2000</div>		Date of mailing of the international search report <div style="text-align: center; font-size: 1.2em;">27.04.00</div>
Name and mailing address of the ISA European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016		Authorized officer <div style="text-align: center; font-size: 1.2em;">Holtorf, S</div>

INTERNATIONAL SEARCH REPORT

Int'l Application No
PCT/EP 99/05652

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	KUSHNIR, S., ET AL.: "characterization of Arabidopsis thaliana cDNAs that render yeasts tolerant toward the thiol-oxidizing drug diamide" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 92, November 1995 (1995-11), pages 10580-10584, XP002127804 see also last paragraph the whole document ---	1,2
Y	WO 96 39020 A (UNIV CALIFORNIA) 12 December 1996 (1996-12-12) the whole document ---	1,2
Y	QUINTERO, F.J., ET AL.: "the SAL1 gene of Arabidopsis, encoding an enzyme with 3' (2'), 5'-bisphosphate nucleotidase and inositol polyphosphate 1-phosphatase activities, Increases salt tolerance in yeast" THE PLANT CELL, vol. 8, March 1996 (1996-03), pages 529-537, XP002092755 see last paragraph the whole document ---	1,2
Y	BABIYCHUK, E., ET AL.: "Arabidopsis thaliana NADPH oxidoreductase homologs confer tolerance of yeasts towards the thiol-oxidizing drug Diamide" THE JOURNAL OF BIOLOGICAL CHEMISTRY, vol. 270, no. 44, 1995, pages 26224-26231, XP002127805 see last paragraph the whole document ---	1,2
Y	GIRAUDAT J ET AL: "ISOLATION OF THE ARABIDOPSIS AB13 GENE BY POSITIONAL CLONING" PLANT CELL, US, AMERICAN SOCIETY OF PLANT PHYSIOLOGISTS, ROCKVILLE, MD, vol. 4, 1 October 1992 (1992-10-01), pages 1251-1261, XP002063682 ISSN: 1040-4651 the whole document ---	1,2
Y	WO 97 41152 A (UNIV NEW YORK) 6 November 1997 (1997-11-06) page 59, line 1 - line 5 ---	1,2
	-/--	

INTERNATIONAL SEARCH REPORT

Int .tional Application No

PCT/EP 99/05652

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	NAMBARA, E., ET AL.: "a mutant of Arabidopsis which is defective in seed development and storage protein accumulation is a new abi3 allele" THE PLANT JOURNAL, vol. 2, no. 4, 1992, pages 435-441, XP002129247 the whole document ----	1,2
A	HELM, K.W. AND VIERLING, E.: "an Arabidopsis thaliana cDNA clone encoding a low molecular weight heat shock protein" NUCLEIC ACID RESEARCH, vol. 17, no. 19, 1989, page 7995 XP002129295 the whole document ----	1,2
A	YANG H ET AL: "Arabidopsis thaliana ECP63 encoding a LEA protein is located in chromosome 4" GENE: AN INTERNATIONAL JOURNAL ON GENES AND GENOMES, GB, ELSEVIER SCIENCE PUBLISHERS, BARKING, vol. 184, no. 1, 3 January 1997 (1997-01-03), pages 83-88, XP004093225 ISSN: 0378-1119 the whole document ----	1,2
A	MIZOGUSHI, T., ET AL.: "characterization of two cDNAs that encode MAP kinase homologues in Arabidopsis thaliana and analysis of the possible role of auxin in activating such kinase activities in cultured cells" THE PLANT JOURNAL, vol. 5, no. 1, 1994, pages 111-122, XP002129296 the whole document ----	1,2
P, X	LEE, J.H., ET AL.: "a highly conserved kinase is an essential component for stress tolerance in yeast and plant cells" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE USA, vol. 96, May 1999 (1999-05), pages 5873-5877, XP002127807 the whole document -----	1,2

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 99/05652

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☒ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
1,2-4,7,8,10-14,16-37 (inventions 1,3,37)
4. ☐ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☒ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claim : 1 completely ; 2 partially

A method to identify cDNAs involved in environmental stress tolerance in plants by expressing a silique-specific cDNA library obtained from said plant in yeast cells and screening the yeast cells for enhanced environmental stress tolerance or resistance.

2. Claims: 5,6,15 completely , 2,3,4,11,12,13,14, 18-37 partially

An isolated cDNA as identified by SEQID 1 coding for a DBF2-related peptide characterized by SEQID 2; furthermore the use of the cDNA in methods to produce transgenic plants with enhanced environmental stress tolerance or resistance.

3. Claims: 10,17 completely , 2,3,4,11,12,13,14, 18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 5 coding for a c74-related peptide characterized by SEQID 6.

4. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 7 coding for a ADH2-related peptide characterized by SEQID 8.

5. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 9 coding for a catalase /catalase3-related peptide characterized by SEQID 10.

6. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 11 coding for a HSP90-related peptide characterized by SEQID 12.

7. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

by SEQID 13 coding for a peptide similar to a phosphoenolpyruvate carboxylase characterized by SEQID 14.

8. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 15 coding for a PR-protein characterized by SEQID 16.

9. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 17 coding for a protein similar to an ascorbate peroxidase characterized by SEQID 18.

10. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 19,21 coding for a protein similar to a phosphatase binding protein characterized by SEQID 20,22.

11. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 23,25 coding for a protein similar to a retinol dehydrogenase characterized by SEQID 24,26.

12. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 27,29 coding for a protein similar to a ribosomal protein characterized by SEQID 28,30.

13. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 31 coding for a protein similar to a protein transporter characterized by SEQID 32.

14. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 33 coding for a protein similar to a peptide transporter characterized by SEQID 34.

15. Claims: 2,3,4,11,12,13,14,18-37 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as invention 2; but limited to the cDNA as identified by SEQID 35 coding for an LCT1-related protein characterized by SEQID 36.

16. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 37 coding for an CYC1-related protein characterized by SEQID 38.

17. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 39 coding for an OSM1-related protein characterized by SEQID 40.

18. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 41 coding for an CUP1-related protein characterized by SEQID 42.

19. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 43 coding for an RAD7-related protein characterized by SEQID 44.

20. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 45 coding for an apocytochrome b-related protein characterized by SEQID 46.

21. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 47 coding for an LPPL1-related protein characterized by SEQID 48.

22. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 49 coding for a protein similar to an auxin binding protein characterized by SEQID 50.

23. Claims: 2,3,4,11,12,13,14,18-37 partially

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

Idem as invention 2; but limited to the cDNA as identified by SEQID 51 coding for an CBP57-related protein characterized by SEQID 52.

24. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 53 coding for a calcineurin B-related protein characterized by SEQID 54.

25. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 55 coding for a calnexin-related protein characterized by SEQID 56.

26. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 57 coding for a calreticulin-related protein characterized by SEQID 58.

27. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 59,61 coding for a calmodulin-related protein characterized by SEQID 60,62.

28. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 63 coding for a DdMek1-related protein characterized by SEQID 64.

29. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 65 coding for an adenosine kinase-related protein characterized by SEQID 66.

30. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 67 coding for a human tyrosine kinase-related protein characterized by SEQID 68.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

31. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 69 coding for an ice-plant tyrosine kinase-related protein characterized by SEQID 70.

32. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 71 coding for a kinase C receptor-related protein characterized by SEQID 72.

33. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 73 coding for a HAT7-related protein characterized by SEQID 74.

34. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 75 coding for a RSEB-related protein characterized by SEQID 76.

35. Claims: 2,3,4,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 77 coding for a phosphatase 2C-related protein characterized by SEQID 78.

36. Claims: 2,3,4,11,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 121 potentially coding for a caltractin-related protein.

37. Claims: 7,8,16 completely; 2,3,11,13,14,18-37 partially

Idem as invention 1; but limited to the cDNA as identified by SEQID 3 coding for a HSP17.6-related protein characterized by SEQID 4.

38. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 79,81 coding for a LEA-related protein characterized by SEQID 80,82.

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39. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 83 coding for a protein similar to a PR-protein characterized by SEQID 84.

40. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 85 coding for a peroxidase-related protein characterized by SEQID 86.

41. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 87 coding for a ribosomal protein characterized by SEQID 88.

42. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 89 coding for a SAS1-related protein characterized by SEQID 90.

43. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 91 coding for a AIG2-related protein characterized by SEQID 92.

44. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 93 coding for a MT1c-related protein characterized by SEQID 94.

45. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 95 coding for a IPP2-related protein characterized by SEQID 96.

46. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 97 coding for a chlorophyll a/b binding protein protein characterized by SEQID 98.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

47. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention ; but limited to the cDNA as identified by SEQID 99 coding for glutathione transferase characterized by SEQID 100.

48. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 101 coding for kin1-related protein characterized by SEQID 102.

49. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 103 coding for Atmpk1-related protein characterized by SEQID 104.

50. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 105 coding for H2A-related protein characterized by SEQID 106.

51. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 107 coding for a protein with unknown function as characterized by SEQID 108.

52. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 109 coding for a protein with unknown function as characterized by SEQID 110.

53. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 111 coding for a protein with unknown function as characterized by SEQID 112.

54. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 113 coding for a protein with unknown function as

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

characterized by SEQID 114.

55. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 115 coding for a protein with unknown function as characterized by SEQID 116.

56. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 117 coding for a protein with unknown function as characterized by SEQID 118.

57. Claims: 2,3,9,11,12,13,14,18-37 partially

Idem as invention 2; but limited to the cDNA as identified by SEQID 119 coding for a protein with unknown function as characterized by SEQID 120.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 99/05652

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